

Fig. 1

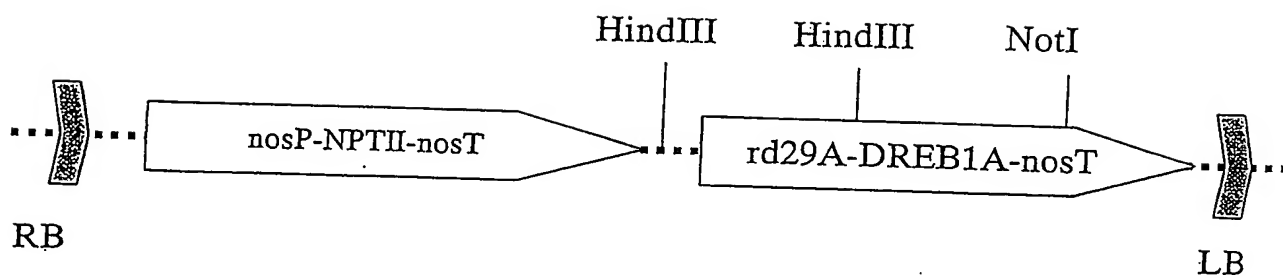


Fig. 2-1

0009114

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Sequence 1 : DREB1A.nuc  
 Size : 651  
 Matching Position : 1 - 651

Sequence 2 : DREB1B.nuc  
 Size : 642  
 Matching Position : 1 - 642

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 85.04 [%]  
 Weight : -451

```

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
***** **** ***** ***** ***** **
1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAG-- -----CC

61 : TC-AGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCGAAGAAAC CGGCGGGTCC
** ***** ** ***** * ** ** ** ***** **
51 : TCAAGGCGGA GATTATTGC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG

120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCCGA GAAACTCCGG
***** ***** ***** ***** ***** * *****
111 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAA GAAACTCCGG

180 : TAAGTGGGTT TGTGAGGTTA GAGAACCAA CAAGAAAACA AGGATTGGC TCGGAACATT
***** * ** * ** ***** ***** ***** **
171 : TAAGTGGGTT TCTGAAGTGA GAGAGCCAA CAAGAAAACC AGGATTGGC TCGGGACTTT

240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTTAGCCC TTCGTGGCCG
***** ***** **** ***** ** ** ***** * *****
231 : CCAAACCGCT GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG

300 : ATCAGCCTGT CTCAATTTTC CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG
***** ** ***** ***** ***** * ** ***** * *****
291 : ATCAGCATGT CTCAACTTTC CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG

360 : CGCTAAGGAC ATCCAAAAGG CGGCGGCTGA AGCTGCGTTG GCGTTTCAGG ATGAGATGTG
*** ***** * **** ***** ** ***** * *****
351 : CGCCAAGGAT ATCCAAAAG CGGCTGCTGA AGCGGCGTTG GCTTTTCAAG ATGAGACGTG

420 : TGATGCGACG ---ACGGATC ATGGCTTCCA CATGGAGGAG ACGTTGGTGG AGGCTATTTA
**** ***** *** ** ***** * ** ***** * *****
411 : TGATACGACG ACCACGAATC ATGGCCTGGA CATGGAGGAG ACGATGGTGG AAGCTATTTA

477 : CACGCGGAA CAGAGCGAA ATGCGTTTTA TATGCAGAT GAGGCGATGT TTGAGATGCC
** ***** ***** ***** ***** * ** ** * **
471 : TACACCGAA CAGAGCGAAG GTGCGTTTTA TATGGATGAG GAGACAATGT TTGGGATGCC

537 : GAGTTTGTG GCTAATATGG CAGAAGGGAT GCTTTTGCCG CTTCCGTCCG TACAGTGAA
** ***** * ***** * ***** ** ***** * ** *****
531 : GACTTTGTG GATAATATGG CTGAAGGCAT GCTTTTACCG CCGCCGTCTG TTCAATGGAA

597 : TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG TTATGGAGTT ATTAA
***** ** * ** * * ** * ** * ** * **

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Fig. 2-2

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591 : TCATAATTAT GACGGCGAAG GAGATGGT-- -GACGTGTG CTTTGGAGTT ACTAA

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Sequence 1 : DREB1A.nuc  
 Size : 651  
 Matching Position : 1 - 651

Sequence 2 : DREB1C.nuc  
 Size : 651  
 Matching Position : 1 - 651

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2

Matching : 86.70 [%]  
 Weight : -476

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC  
 \*\*\*\*\* \*\* \*\*\*\*\* \* \*\*\*\*\*

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC

61 : TCAGGCGGTG ATTATATTCC GACGCTTGCG AGCAGCTGCC CCAAGAAACC GGCGGGTCTG  
 \*\*\*\*\* \*

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATA TACAGAGGAG TTCGTGGGAG AAACCTCCGGT  
 \*\*\*\*\* \*

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAGAAAACAA GGATTGGCT CGGAACATTT  
 \*\*\*\*\* \*

181 : AAGTGGGTTT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC

241 : CAAACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTTTAGCCCT TCGTGGCCGA  
 \*\*\*\*\* \*

241 : CAAACCGCTG AGATGGCAGC TCGTGTCTAC GACGTCGCCG CCATAGCTCT CCGTGGCAGA

301 : TCAGCCTGTC TCAATTTTCG TGACTCGGCT TGGAGACTCC GAATCCCGGA ATCAACTTGC  
 \*\* \*\*\*\*\* \*

301 : TCTGCCTGTC TCAATTTTCG TGACTCGGCT TGGCGGCTAC GAATCCCGGA ATCAACTGT

361 : GCTAAGGACA TCCAAAAGGC GGCGGCTGAA GCTGCGTTGG CGTTTCAGGA TGAGATGTGT  
 \*\* \*\*\*\*\* \*

361 : GCCAAGGAAA TCCAAAAGGC GGCGGCTGAA GCCGCGTTGA ATTTTCAAGA TGAGATGTGT

421 : GATGCGACGA CGGA---TCA TGGCTTCGAC ATGGAGGAGA CGTTGGTGGG GGCTATTTAC  
 \*\* \*\*\*\*\* \*

421 : CATATGACGA CGGATGCTCA TGGTCTTGAC ATGGAGGAGA CTTTGGTGGG GGCTATTTAT

478 : ACGGCGGAAC AGAGCGAAAA TGCCTTTTAT ATGCACGATG AGGCGATGTT TGAGATGCCG  
 \*\*\* \*\*\*\*\* \*

481 : ACGGCGGAAC AGAGCCAAGA TGCCTTTTAT ATGGATGAAG AGGCGATGTT GGGGATGTCT

538 : AGTTTGTGG CTAATATGGC AGAAGGGATG CTTTTCGCCG TTCCGTCCGT ACAGTGAAT  
 \*\*\*\*\* \*

541 : AGTTTGTGG ATAACATGGC CGAAGGGATG CTTTACCGT CGCCGTCGGT TCAATGGAAC

Fig. 2-3

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598 : CATAATCATG AAGTCGACGG CGATGATGAC GACGTATCGT TATGGAGTTA TTAA
      ***** ** * ***** ** ***** ***** ** * ***** ** ****
601 : TATAATTTTG ATGTCGAGGG AGATGAT--- GACGTGTCCT TATGGAGCTA TTAA

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Sequence 1          : DREB1A.nuc
  Size              : 651
  Matching Position : 1 - 651

Sequence 2          : DREB1D.nuc
  Size              : 675
  Matching Position : 1 - 675

Matching Condition.

Matches             : -1
Mismatch            : 1
Gaps                : 1
#Nt                 : 2

Matching            : 68.72 [%]
Weight              : -233

1 : ATGAACTCAT TT---TCTGC TTTTCTGAA ATGTTT----- --GGCTCCGA TTACGAGTCT
    ***** ** * ***** ** ***** ***** ** * *****
1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : TCGGTTTCCT CAGGCGGTGA TTATATTCGG ACGCTTGCGA GCAGCTGCCC CAAGAAACCG
    ***** * ***** * * * * * * * * * * * * * * * * * * * * * *
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

112 : GCGGGTCGTA AGAAGTTTCG TGAGACTCGT CACCCAATAT ACAGAGGAGT TCGTCGGAGA
    ** ** * * ***** ***** ** * * * * * * * * * * * * * * * *
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

172 : AACTCCGGTA AGTGGGTTTG TGAGGTTAGA GAACCAAACA AGAAAACAAG GATTTGCTC
    ** ** ***** * ***** ** * * * * * * * * * * * * * * * *
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTGGTTA

232 : GGAACATTTT AAACCGCTGA GATGGCAGCT CGAGCTCAGC ACGTTGCCGC TTTAGCCCTT
    ** ** ***** ** * * * * * * * * * * * * * * * * * * * * *
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCCGAT CAGCCTGTCT CAATTTGCTT GACTCGGCTT GGAGACTCCG AATCCCGGAA
    ***** ** * * ***** ***** ** * * * * * * * * * * * * *
301 : CGTGGTCGCT CTGCTTGTCT CAATTTGCTT GATTCTGCTT GCGGCTTCG TATTCTGAG

352 : TCAACTTGCG CTAAGGACAT CCAAAGGCG GCGGCTGAAG CTGCGTTGGC GTTTCAGGAT
    * ***** ***** ** ** * * * * * * * * * * * * * * * *
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTGAT- ----GCGACG ACGGA-TCA- TGGCTTCGAC A-TGGAGGAG
    **** * * * * * * * * * * * * * * * * * * * * * * * * *
421 : GAGACTACGA CGGAGGGATC TAAACTGCC GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

457 : ACGTTGGTGG AGGCTATTTA CACGGCGGAA CAGAGCGAAA ATGCGTTTTA TATGCACGAT
    * ** * * * * * * * * * * * * * * * * * * * * * * * * *
481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT

517 : GAGGCGATGT TTGAGATGCC GAGTTTGTG GCTAATATGG CAGAAGGGAT GCTTTTGCCG
    ***** * * * * ***** * ** * * * ***** * ** *****
541 : GAGGCGCTTT TGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG
  
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Fig. 2-4

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577 : CTTCGTCGG TACAGTGGAA TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG  
 \* \*\*\* \* \* : \*\*\*\*\* \* \*\* \* \*\*\*\* \* \* \* \* \*\*\*\*\* \*\*  
 601 : CCGCCGGAAG TTGGCTGGAA TCATA---AC GACTTTGACG GAG-TG--GG TGACGTGTCA

637 : TTATGGAGTT -----ATTA A  
 \* \*\*\*\*\* \* \* \*  
 655 : CTCTGGAGTT TTGACGAGTA A

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Sequence 1 : DREB1A.nuc  
 Size : 651  
 Matching Position : 1 - 651

Sequence 2 : DREB1E.nuc  
 Size : 546  
 Matching Position : 1 - 546

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 54.70 [%]  
 Weight : 0

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTC-  
 \*\*\* : \*\*\*\* : \*\*\*\* : \*\* \* \*\*  
 1 : ATG----- ----GAAA-- ----ACGA-- --CGATATCA  
 60 : CTCAGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCCAAGAAAC CGGCGGGTGC  
 \* \*\*\*\*\* \*\* : \* \*\* \*\* \*\*\*\*\* \* \*\* \* \*\*  
 20 : CCGTGGCGGA GAT----- ----GAG----- CCAAAGAAGC GTGCTGGACC  
 120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCGGA GAAACTCCGG  
 \* \*\* \*\* \*\*\*\*\* \* \*\*\*\*\* \*\*\*\*\* \*\* \*\* \* \*\* \* \*\* \* \*\*  
 57 : GAGGATTTTC AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA  
 180 : TAAGTGGGTT TGTGAGGTTA GAGAACCAAA CAAGAAAACA AGGATTTGGC TCGGAACATT  
 \*\* \*\*\*\*\* \*\* \*\* \* \* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\* \*  
 117 : CAAATGGGTA TGCGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACTTA  
 240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTTAGCCC TTCGTGGCCG  
 \*\* \*\* \*\* \*\* \*\*\*\*\* \* \* \*\* \*\*\*\*\* \*\*\*\*\* \* \* \* \* \* \* \* \* \*  
 177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGGAG  
 300 : ATCAGCCTGT CTCAATTTCT CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG  
 \*\*\* \*\* \*\* \* \*\*\*\*\* \* \*\* \*\* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\*  
 237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCGG CATCCACT--  
 360 : CGCTAAGGAC ATCCAAAAGG ----CGGCGG CTGAAGCTGC GTTGGCGTTT CAGGATG-AG  
 \* \* \*\*\*\* \* \* \* \*\*\*\*\* \* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\* \*  
 295 : -GATCCGGAC A-CGATCAGG CGCACGGCGG CCGAAGCAGC GGAGATG-TT CAGGCCGCCG  
 415 : ATGTGTGATG CGACGACGGA TCATGGCTTC GACATGGAGG AGACGTTGGT GGAGGCTATT  
 \*\* \* \* \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 352 : GAGT-TTAGT --AC-AGGAA TTACGGTTTT ACCCT----C AGCC---AGT -GAG---TTT  
 475 : TACACGGCGG AACAGAGCGA AAATGCCGTTT TATATGCACG ATGAGGCGAT GTTTGAGATG

Fig. 2-5

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397 : ***** * * ** * * * * * * * * * * * * * * * *
      GACACGTCGG A--TGA---A GGAGTCGCTG GA-ATG-ATG ATGAGGC--T CGCGGAGGAG

535 : CCGAGTTTGT TG--GCTAAT ATGGCAGA-A GGGATGCTTT TGCCGCTTCC GTCCGTACAG
      ***      * * * * * * * * * * * * * * * * * * * * *
448 : CCGTTGATGT CGCCGCCAAG ATCGTACATT GATATG-AAT --ACG----A GTGTGTAC-G

592 : TGGAATCATA ATCATGAAGT CGACGGCGAT GATGACGACG TATCGTTATG GAGTTATTAA
      **** * * * *** * * * * * * * * * * * * * * * *
500 : TGGACGAAGA A--ATG-----TGT TACGAAGATT TGTCACTTTG GAGTTACTAA

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```
Sequence 1      : DREB1A.nuc
Size           : 651
Matching Position : 1 - 651
```

```
Sequence 2      : DREB1F.nuc
Size           : 630
Matching Position : 1 - 630
```

**Matching Condition.**

```
Matches      :    -1
Mismatches   :     1
Gaps         :     1
*N+         :     2

Matching     :    54.81 [%]
Weight       :   -21
```

```

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
**** * * ** **
1 : ATGAA----- ----TAATG AT-----G AT----- ----ATTAT

61 : TCAGGCGGTG ATTATATTCC GACGCTTGCG AGCAGCTGCC CCAAGAAACC GCGGGTTCGT
** ***** * ** * * * ***** * ***** *
21 : TCTGGCGGAG AT----- ----G A-----GCG CTAAGAAGCG TCGGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATA TACAGAGGAG TTCGTCGGAG AAACCTCCGT
* **** ***** ** ***** * ***** * * ***** ** *
58 : AGAGTGTTTA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAGAAAACAA GGATTGCGT CGGAACATTT
** ***** * * ** ** ** ***** * * ** * ***** ** ** *
118 : AAATGGGTCT GCGAAGTCAG AGAACCGACG CACCAACGCC GCATTGCGT CGGGACTTAT

241 : CAAACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTTTAGCCCT TCGTGGCCGA
* ** ** * * ***** ** ** ** ***** ** * ***** **
178 : CCCACAGCAG ATATGGCAGC GCGTGACACG GACGTGGCGG TTTAGCTCT GCGTGGGAGA

301 : TCAGCCTGTC TCAATTTGCG TGACTCGGCT TGGAGACTCC GAATCCCGGA ATCAACTTGC
** ** ** * ***** ***** ** ** * ** * * ***** ** *
238 : TCCGCATGTT TGAATTTGCG CGACTCGGCT TGGCGGCTTC CGGTGCCGGA ATCCAATGAT

361 : GCTAAGGACA TCCAAAAGGC GCGGCTGAA GCTGCGTTGG CGTTTCAGGA TG--AGATGT
* * * * * ** * ***** ** ***** * **** ** * *** *
298 : CCGGATGTGA TAAGAAGAT TCGCGCGGAA GCTGCGGAGA TGTTC-AGGC CGGTGGATT

419 : -GTGA-TGCG ACGACGGATC ATGGCTT--- --CGACATGG AGGAGACGTT GGTGGAGGCT
* * ** * **** * ** ** ** * ** * * ** * **
357 : AGAAAGTGGA ATTACGG-TT TTGCCTTGTG CGGGAGATGA TGTGGATTG GGTTTTGGTT

```

Fig. 2-6

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472 : ATTTACACGG C----- GGAACAGA-G CGA-AAATGC GT-TTTATAT GCACGATGAG
      *** *          *** * * * * * * * * * * * * * * * *
416 : CGGGTTCCGG CTCTGGTTCG GGATCGGAGG AGAGGAATTC TTCTTCGTAT GGATTGGAG

520 : GCGATGTTTG AGATGCCGAG TTTGTTGGCT AATATGGCAG AAGGGATGCT TTTGCCGCTT
      * * * * * * * * * * * * * * * * * * * * * *
476 : ACTACG-AAG AAGTCTCAAC GACGATGATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

580 : C--CGTCCGT ACAGTGGAA- -----TCA TAATCATG-- -AAGTCGACG --GCGATG--
      * * * * * * * * * * * * * * * * * * * * * *
535 : CCGCGATCGT ATA-TGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

623 : --ATGACGAC GTATCGTTAT GGAGT----- -TATTAA
      **** * * * * * * * * * * * * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA

```

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```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

```

```

Sequence 2      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*NT+             : 2

```

```

Matching          : 86.33 [%]
Weight            : -471

```

```

1 : ATGAACTCAT TTTAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TC-----
   ***** * * * * * * * * * * * * * * * *
1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC

53 : -AAGGCGGAG ATTATTGTCC GACGTTGGCC ACGAGTTGTC CGAAGAAACC GGCGGGCCGT
     ***** * * * * * * * * * * * * * * * *
61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG

112 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT
      ***** * * * * * * * * * * * * * * * *
121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT

172 : AAGTGGGTTT CTGAAGTGAG AGAGCCAAAC AAGAAAACCA GGATTGGCT CGGGACTTTC
      ***** * * * * * * * * * * * * * * * *
181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC

232 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCTG CATTAGCCCT CCGTGGCCGA
      ***** * * * * * * * * * * * * * * * *
241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCGG CCATAGCTCT CCGTGGCAGA

292 : TCAGCATGTC TCAACTTCGC TGAATCGGCT TGGCGGCTAC GAATCCCGGA GTCAACATGC
      ** * * * * * * * * * * * * * * * *
301 : TCTGCCTGTC TCAATTTGCG TGAATCGGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT

352 : GCCAAGGATA TCCAAAAGC GGCTGCTGAA GCGGCGTTGG CTTTTCAAGA TGAGACGTGT
      ***** * * * * * * * * * * * * * * * *

```

Fig. 2-7

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361 : GCCAAGGAAA TCCAAAAGGC GCGGCTGAA GCCGCGTTGA ATTTTCAAGA TGAGATGTGT
412 : GATACGACGA CCACGAATCA TGGCCTGGAC ATGGAGGAGA CGATGGTGA AGCTATTTAT
    *** ***** *      *** ** * ** ***** * ***** *****
421 : CATATGACGA CGGATGCTCA TGGTCTTGAC ATGGAGGAGA CCTTGGTGA GGCTATTTAT

472 : ACACCGGAAC AGAGCGAAGG TGCCTTTTAT ATGGATGAGG AGACAATGTT TGGGATGCCG
    ** ***** ***** *** ***** ***** * ** * ***** *****
481 : ACGCCGAAC AGAGCCAAGA TGCCTTTTAT ATGGATGAAG AGGCGATGTT GGGGATGTCT

532 : ACTTTGTTGG ATAATATGGC TGAAGGCATG CTTTACCAGC CGCCGTCTGT TCAATGGAAT
    * ***** **** ***** ***** *** ***** ***** ** *****
541 : AGTTTGTGTTG ATAACATGGC CGAAGGGATG CTTTACCAGT CGCCGTCTGT TCAATGGAAC

592 : CATAATTATG ACGCGGAAGG AGATGGTGAC GTGTCGCTTT GGAGTTACTA A
    ***** ** * * ** * ***** ***** * * **** * * *
601 : TATAATTTTG ATGTCGAGGG AGATGATGAC GTGTCCTTAT GGAGCTATTA A
  
```

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```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642
  
```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*NT              : 2

Matching          : 68.88 [%]
Weight            : -234
  
```

```

1 : ATGAACTCAT TT---TCAGC TTTTCTGAA ATGTTT---- --GGCTCCGA TTA-CGAGC-
    ***** ** * * * * * * * * ***** ***** * * *
1 : ATGAATCCAT TTTACTCTAC ATTCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

50 : -----CTC AAGGCGGAGA TTATTGTCGG ACGTTGGCCA CGAGTTGTCC GAAGAAACCG
    * * * * * * * * * * * * * * * * * * * * * *
61 : CCGGTTTCAG ACAGTAGTA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

103 : GCGGGCCGTA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
    ** ** * * ***** ***** *** ** * **** ***** ***** **
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

163 : AACTCCGGTA AGTGGGTTTC TGAAGTGAGA GAGCCAAACA AGAAAACCAG GATTTGGCTC
    ** ** **** * ***** ***** *** ***** ** * ***** * * *****
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA

223 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCAGC ACGTCGCTGC ATTAGCCCTC
    ** ***** * ** * *** ***** *** ***** * * * ***** *****
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

283 : CGTGGCCGAT CAGCATGTCT CAATTCGCT GACTCGGCTT GCGGGCTACG AATCCCGGAG
    ***** ** * * * * * * * * ***** ** * * **** ***** ** * * *
301 : CGTGGTCGCT CTGCTTGCT CAATTCGCT GATTCTGCTT GCGGGCTTCG TATTCCTGAG
  
```

Fig. 2-8

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343 : TCAACATGCG CCAAGGATAT CCAAAAAGCG GCTGCTGAAG CGGCGTTGGC TTTTCAAGAT
      * * * * *
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

403 : GAGAC----- --GTGTGA-- TACGACGACC AC-GAATCA- TGGCCTGGAC A-TGGAGGAG
      *****
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

451 : ACGATGGTGG AAGCTATTTA TACACCGGAA CAGAGCGAAG GTGCGTTTTA TATGGATGAG
      ** * * *
481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT

511 : GAGACAATGT TTGGGATGCC GACTTTGTTG GATAATATGG CTGAAGGCAT GCTTTTACCG
      *** * * *
541 : GAGGCGCTTT TGGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG

571 : CCGCCGCTCG TTCAATGGAA TCATAATTAT GACGGCGAAG GAGATGGTGA CGTGTGCTT
      *****
601 : CCGCCGGAAG TTGGTGGAA TCATA---AC GACTTTGACG GAGTGGGTGA CGTGTCACTC

631 : TGGAGTT--- ---ACTAA
      *****
658 : TGGAGTTTTG ACGAGTAA
  
```

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```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642
  
```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 53.38 [%]
Weight            : 2
  
```

```

1 : ATGAACTCAT TTTAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGGCGGA
   ***
1 : ATG----- -GAAA-- -ACGACG AT---ATCA CCGTGGCGGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG TAAGAAGTTT
   ***
30 : GAT----- -GA----- -AG----- CCAAGAAGC GTGCTGGACG GAGGATTTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
     *****
67 : AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA CAAATGGGTA

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTGGC TCGGGACTTT CCAAACCGCT
     * * * * *
127 : TGCGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACCTA TCCGACGGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG ATCAGCATGT
     ** * * *
187 : GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TGCGCGGGAG ATCCGCGTGT
  
```

Fig. 2-9

0009114

```

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAAC--A TCGCCCAAGG
    * ** * * * * * * * * * * * * * * * * * * * * * * * * * *
247 : TTGAATTCTT CCGATTCTGC TTGGAGGTTG CCGGTGCCCG CATCCACTGA TCCGGACACG

359 : AT-ATCCAAA AAGCGGCTGC TGAAGCGGCG TTGGCTTTTC AAGATG-AGA CGTGTGATAC
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
307 : ATCAGGCGCA ---CGGCGGC CGAAGCAGCG -GAGATGTT AGGCCGCCGG AGTTTAGTAC

417 : GACGACCACG AATCATGGCC T-GGACATGG AG---GAGAC GATGGTGGAA GCTATTATA
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
363 : AGGAATTACG -GTTTACCC TCAGCCAGTG AGTTTGACAC GTCGGATGAA G-----GAGT

473 : CACCGGAACA GAGCGAAGGT GCGTTTTATA TGGATGAGGA GACAATGTTT GGGATGCCGA
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
417 : CGCTGGAA-- ---TGATGAT GAG-----GC TCGCGGAGGA GCCGTTGATG TCGCCGCCAA

533 : CTTTGTGGGA TAATATGGCT GAAGGCATGC TTTTACCGCC GCCGTCTGTT CAATGGAATC
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
467 : GATCGTACAT TGATA----T GAA----- ---TAC---- -GAGTGTGA C-GTGGACGA

593 : ATAATTATGA CGGCGAAGGA GATGGTGACG TGTCGCTTTG GAGTTACTAA
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
507 : AGAAATGTG- TTACGAA--- -----GATT TGTCACCTTG GAGTTACTAA

```

+++++

```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

## Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
* N +            : 2

Matching          : 56.23 [%]
Weight            : -34

```

```

1 : ATGAACTCAT TTTCAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGCGCGA
    ***** * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGAA-TAAT GATGATATTA TTCT----- -----GCGCGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG TAAGAAGTTT
    *** * * * * * * * * * * * * * * * * * * * * * * *
30 : GAT----- ---GA---GG CCTAAGAAGC GTGCGGGAAG GAGAGTGTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
    ***** * * * * * * * * * * * * * * * * * * * * *
67 : AAGGAGACAC GTCACCCAGT TTACAGAGGC ATAAGCGGGA GGAACGGTGA CAAATGGGTC

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTGGC TCGGGACTTT CCAAACCGCT
    * * * * * * * * * * * * * * * * * * * * * * * * * *
127 : TGCGAAGTCA GAGAACCACG GCACCAACGC CGCATTGGC TCGGGACTTA TCCCACAGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG ATCAGCATGT

```

Fig. 2-10

0009114

```

187 : ** ***** * ***** ** ***** ** * ***** * * ***** * *** *****
      GATATGGCAG CGCGTGCACA CGACGTGGCG GTTTTAGCTC TCGTGGGAG ATCCGCATGT

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG CGCC-AAGGA
      * ** **** * ***** ** ***** * * **** * ** * *** ** * *

247 : TTGAATTCG CCGACTCCGC TTGGCGGCTT CCGGTGCCG AATCCA-ATG ATCCGGATGT

360 : TATCCAAAAA GCGGCTGCTG AAGCGGCGTT GGCTTTTCAA GATGAGACGT GTGATACGAC
      ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *

306 : GATAAGAAGA GTTGGCGCGG AAGCTGCGGA GATGTTTAGG CCGGTGGATT TAGAAAGTGG

420 : GACCACGAAT ----CATGGC CTGGACATG- -GAGGA---- GACGATGGT- --GG---AAG
      * *** * * * * * * * * * * * * * * * * * * * * * * * * *

366 : AATTACGGTT TTGCCTTG TGCGGAGATGA TGTGGATTTG GGTTTTGGTT CCGGTTCCGG

464 : CTAT--TTAT ACACCGGAAC AGAGCGAAGG TCGGT-TTTA TATGGATGAG GAGACAATGT
      ** * ** * * **** * * * * * * * * * * * * * * * * * * * * *

426 : CTCTGGTTTG GGATCGGAGG AGAG-GAA-- TTCTTCTTCG TATGGATTTG GAGACTACG-

521 : TTGGGATGCC GACTTTGTTG GATAATA-TG GCTGAAGG-- CA-TGCTTTT ACCGCCGC--
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

482 : AAGAAGTCTC AACGACGAT- GATGAGACTC GCGGAGGGGC CACTAATGTC GCCGCCGCGA

575 : -CGTCTGTTT AA---TGGAA TCATAATTAT G-----ACGG CGAAGGAGAT G-GT-----
      *** * * * * * * * * * * * * * * * * * * * * * * * * * *

541 : TCGTATATGG AAGACATGAC TCCTACTAAT GTTTACACGG AAGAAGAGAT GTGTTATGAA

619 : GACGTGTCGC TTTGGAGTTA C-----TAA
      ** **** * ***** * * *

601 : GATATGTCAT TGTGGAGTTA CAGATATTAA
  
```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651
  
```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
#N+          : 2

Matching      : 68.34 [%]
Weight       : -233
  
```

```

1 : ATGAACTCAT TT---TCTGC CTTTCTGAA ATGTTT---- --GGCTCCGA TTACGAGTCT
      ***** ** * * * * * * * * * * * * * * * * * * * * * *

1 : ATGAATCCAT TTTACTCTAC ATTCCAGAG TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : CCGGTTTCTT CAGGCGGTGA TTACAGTCCG AAGCTTGCCA CGAGCTGCC CAAGAAACCA
      ***** * **** * ** *** * ** * ** * * * * * * * * * *

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

112 : GCGGGAAGGA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
      ** ** **** * * * * * * * * * * * * * * * * * * * * * *

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
  
```

Fig. 2-11

0009114

```

172 : AACTCCGGTA AGTGGGTGTG TGAGTTGAGA GAGCCAAACA AGAAAACGAG GATTTCGGCTC
    ** ** ** * ** ** * ** * ** * ** * ** * ** * ** * ** * **
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTCGGTTA

232 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCAGC ACGTCGCCGC CATAGCTCTC
    ** ** ** * ** * ** * ** * ** * ** * ** * ** * ** * **
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCAGAT CTGCCTGTCT CAATTCGCT GACTCGGCTT GCGGCTACG AATCCCGGAA
    ***** * ** * ** * ** * ** * ** * ** * ** * ** * **
301 : CGTGGTCGCT CTGCTTGTCT CAATTCGCT GATTCTGCTT GCGGCTTCG TATTCCTGAG

352 : TCAACCTGTG CCAAGGAAAT CCAAAAGGCG GCGGCTGAAG CCGCGTTGAA TTTTCAAGAT
    * ** * ** * ** * ** * ** * ** * ** * ** * ** * **
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTCATA TGA-----CG ACGGATGCTC ATGGTCTTGA CA-TGGAGGA
    **** : * * * * * * * * * ** **** * * * * * **
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG A-GGAGGCGG CAGGGGAGGG

459 : GACCTTGGTG GAGGCTATTT ATACGCCGGA ACAGAGCCAA GATGCGTTTT ATATGGATGA
    * ** * ** * ** * ** * ** * ** * ** * ** * **
480 : GGTGAGGGAG GGGAGAGGA GGGCGGAGGA GCAGAATGGT GGTGTGTTTT ATATGGATGA

519 : AGAGGCGATG TTGGGGATGT CTAGTTTGTG GGATAACATG GCCGAAGGGA TGCTTTTACC
    ***** * ***** * * ** * ** * ** * ** * ** * **
540 : TGAGGCGCTT TTGGGGATGC CCAACTTTTT TGAGAATATG GCGGAGGGGA TGCTTTTGCC

579 : GTCCCGCTCG GTTCAATGGA ACTATAATTT TGATGTCGAG GGAGATGATG ACGTGTCTTT
    * ***** ** * ** * ** * ** * ** * ** * ** * **
600 : GCCGCCGGA GTTGGCTGGA ATCATAA--- CGACTTTGAC GGAGTGGGTG ACGTGTCACT

639 : ATGGAG---- --CTATTAA
    ***** * * **
657 : CTGGAGTTTT GACGAGTAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N +       : 2

Matching      : 54.95 [%]
Weight       : 1

```

```

1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC
    ***                **** * ** * ** * **
1 : ATG----- -----GAAA-- ----ACGACG AT-----ATC ACCG-----

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ***** * **                * * ***** * ** * **

```



Fig. 2-12

0009114

```

23 : --TGGCGGAG AT----- GAAG----- -----C CAAAGAAGCG TGCTGGACGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT
      * ** **      ***** ** ***** ***** * * ** * ** ** **
58 : AGGATTTTCA AGGAGACACG TCACCCAATC TACAGAGGCG TCGGGCGTAG GGACGGCGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGA-TTTGGC TCGGGACTTT
      ** ***** * ** * * ** ** * * * ** * ** * ** * **
118 : AAATGGGTAT GCGAAGTCCG TGAACCGATT CA-TCAGCGT CGAGTCTGGC TCGGAACCTA

240 : CCAAACCGCT GAGATGGCAG CTCGTGCTCA CGACGTGCGC GCCATAGCTC TCCGTGGCAG
      * ** ** * ** ***** * ***** ***** ** * * **** * ** **
177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGGAG

300 : ATCTGCCTGT CTCAATTTTC CTGACTCGGC TTGGCGGCTA CGAATCCCGG AATCAACCTG
      *** ** ** * ***** * ** ** * ** ** * * * * **** * **
237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCCG CATCCA-CTG

360 : TGCCAAGGAA ATCCAAAAGG ----CGGCGG CTGAAGCCGC GTTGAATTTT CAAGATGAGA
      ** *** * * * ** ***** * ***** ** * * ** ** *
296 : ATCC--GGAC A-CGATCAGG CGCACGGCGG CCGAAGCAGC GGAG-ATGTT CAGGCCG-CC

416 : TGTGTCATAT GACGACGGAT GCTCATGGTC TTGACATGGA GGAGACCTTG GTGGAGGCTA
      * ** ** ** *** * * *** ** * * ** ** * **
351 : GGAGT-TTAG TAC--AGGA- -ATTACGGTT TTACCCT--- -CAG-CC--A GT-GAG---T

476 : TTTATACGCC GGAACAGAGC CAAGATGCGT TTTATATGGA TGAAGAGGCG ATGTTGGGGA
      ** * *** * *** ** * ** * * * ** * ** * ** * **
395 : TTGACACGTC GGA--TGA-- -AGGAGTCGC TGGA-AT-GA TGATGAGGC- ---TCGCGGA

536 : TGTCTAGTTT GT-TGGATAA CATGGCCGAA GGGATGCTTT TACCGTCGCC GTCGGTTCAA
      * *** * ** * ** * ** * ** * * * * ** **
444 : GGAGCCGTTG ATGTCGCCGC CAAGATCGTA -CATTGATAT GA--ATACGA GTGTGTAC-G

595 : TGGAACATA ATTTTGATGT CGAGGGAGAT GATGACGTGT CCTTATGGAG CTATTAA
      **** * * * **** * * ** ** * ** * * ** * **
500 : TGGACGAAGA A-----ATGT -----GTTAC GAAGATTTGT CACTTTGGAG TTAATAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 56.10 [%]
Weight          : -35

```

```

1 : ATGAACATCAT TTTCTGCCTT TTCTGAAATG TTGGCTCCG ATTACGAGTC TCCGGTTTCC
    *****          **** *          * **          **
1 : ATGAA----- -----TAATG AT-----G AT-----ATTAT

```

Fig. 2-13

0009114

```

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ** ***** **
21 : TCTGGCGGAG AT----- --GA---GGC CTAAGAAGCG TCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAAGTCCGGT
    * **** ***** ** ***** * * * ** *
58 : AGAGTGTTTA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC
    ** ***** * * * * * * * * * * * * * * *
118 : AAATGGGTCT GCGAAGTCAG AGAACCAGCG CACCAACGCC GCATTGGCT CGGGACTTAT

241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTGCGCG CCATAGCTCT CCGTGGCAGA
    * * * * * * * * * * * * * * * * * * *
178 : CCCACAGCAG ATATGGCAGC GCGTGCACAC GACGTGGCGG TTTAGCTCT GCGTGGGAGA

301 : TCTGCCTGTC TCAATTTGCG TGACTCGGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT
    ** * * * * * * * * * * * * * * * * * *
238 : TCCGCATGTT TGAATTTGCG CGACTCCGCT TGGCGGCTTC CGGTGCCGGA ATCCAATGAT

361 : GCCAAGGAAA TCCAAAAGGC GCGCGGTGAA GCCGCGTTGA ATTTTCAAGA TG--AGATGT
    * * * * * * * * * * * * * * * * * * *
298 : CCGGATGTGA TAAGAAGAGT TCGGGCGGAA GCTGCGGAG- ATGTTTAGGC CGGTGGATT

419 : GTCATATG-- ACGACGGATG CTCATGGT-C TTGACATG-- GAGGA----G ACCTTGGTGG
    * * * * * * * * * * * * * * * * *
357 : AGAAAGTGA ATTACGGTTT TGCCTTGTC GGGAGATGAT GTGGATTGG GTTTTGGTTC

470 : AGGCTATTTA TACG---CCG GAACAGAGCC AAG--ATGCG T-TTTATATG GATGAAGAGG
    * * * * * * * * * * * * * * * * *
417 : GGGTTCGGC TCTGGTTCGG GATCGGAGGA GAGGAATTCT TCTTCGTATG GATTGGAGA

524 : CGATGTTGGG GATGTCTAGT TTGTTGGATA ACA-TGGCCG AAGGGATGCT TTTACCGTCG
    * * * * * * * * * * * * * * * * *
477 : CTACGAAGAA G-TCTCAACG ACGAT-GATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

583 : CCGTCCGT-- TCAATGGAA- -----C TA-TAATTTT GATGTCGAGG --GAGATG--
    *** * * * * * * * * * * * * * * *
535 : CCG-CGATCG TATATGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

626 : --ATGACG-- -TGTCCTTAT GG-----AG CTATTAA
    **** * **** * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA
  
```

+++++

```

Sequence 1      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps             : 1
*N+              : 2

Matching         : 51.26 [%]
Weight           : 29
  
```

Fig. 2-14

0009114

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
   ***                               **          ** * *** *      ***
1 : ATG-----GA-----AAACGACGA T-----ATCA

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
   ** ** * * *      **          * *** ** ***** **
20 : CC-GTGGCGG A-----GA-----T GAAG----CC AAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
   ***** ** ** ***** ** ** * * ***** ** ** * ***
49 : GCTGGACGGA GGATTTTCAA GGAGACACGT CACCCAATCT ACAGAGGCGT GCGGCGTAGG

181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAATCTAG GATTGGTTA
   * * * ***** ** ***** * ** * * * * * * * * * *
109 : GACGGCGACA AATGGGTATG CGAAGTCCGT GAACCGATTG ATCAGCGTCG AGTCTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
   ** **** ** ***** ** ***** ** ***** * * * * * * * *
169 : GGAAC TTATC CGACGGCAGA TATGGCCGCA CGTGCTCAGC ACGTGGCGGT TCTTGCTCTG

301 : CGTGGTCGCT CTGCTTGCTT CAATTTCTGCT GATTCTGCTT GGCGGCTTCG TATTCCTGAG
   ** ** * * * * * * * * * * * * * * * * * * * * * * * *
229 : CGCGGGAGAT CCGCGTGTG GAATTTCTCC GATTCTGCTT GGAGGTTGCC GGTGCCGGCA

361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT
   * *** ** * * * * * * * * * * * * * * * * * * * *
289 : TCCACTGATC CGGACACGAT CAGGCGCAGC GCGGCCGAAG CAGCGGAGAT G-TTCAG---

421 : GAGACTACGA CGGAGGGATC TAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG
   ** ***** * ** * * * * * * * * * * * * * * * *
345 : -----GCCGC CGGAG---TT TAGTACAG-G AATTA--CGG TTTACCCTC A-GCCAGTGA

481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGATGAT
   ** * * * * * * * * * * * * * * * * * * * * * *
393 : GTTTGACACG TCG-GATGAA GGAGTCGCTG --GAATGATG ATGAG----- GCTCGCGGAG

541 : GAGGCGCTTT TGGGATGCC CAACTTTTTT GAGAATATGG CCGAGGGGAT GCTTTTGCCG
   *** ** * * * * * * * * * * * * * * * * * * * *
445 : GAGCCGTTGA TGTGCGCGCC AAGATCGTAC ATTGATAT-- ----GAAT' ACGAGT---

601 : CCGCCGGAAG TTGGCTGGAA TCATAACGAC TTTGACGGAG TGGGTGACGT GTCACCTGG
   * * * * * * * * * * * * * * * * * * * * * *
494 : ----TGACG TGGAC--GAA --GAAATG-- TGTACGAA- ----GATT GTCACCTGG

661 : AGTTTTGACG AGTAA
   **** * ***
538 : AGTT----- ACTAA

```

+++++

```

Sequence 1      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

Fig. 2-15

0009114

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
* N+         : 2

Matching     : 54.92 [%]
Weight       : -24

```

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
   *****                               *** ** * *** *
1 : ATGAAT----- -AAT-----GA TGATATTATT

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
   * ** * * * * *** * ** ***** **
22 : CTGG---CGG AGA---TGA -----GGCC TAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
   ** ** ***** **** ***** ** ** *** ***** * * * ****
49 : GCGGGAAGGA GAGTGTTTAA GGAGACACGT CACCCAGTTT ACAGAGGCAT AAGGCGGAGG

181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA
   ** ** * ***** ** ***** ** ** * * ** * * ***** *
109 : AACGGTGACA AATGGGCTCG CGAAGTCAGA GAACCGACGC ACCAACGCCG CATTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
   ** ***** ** * * * * ** ***** ** ***** ** * * * * * *****
169 : GGGACTTATC CCACAGCAGA TATGGCAGCG CGTGACACAG ACGTGGCGGT TTTAGCTCTG

301 : CGTGGTCBCT CTGCTTGCTT CAATTTGCTT GATTCTGCTT GCGGGCTTCG TATTCCTGAG
   ***** * * * * * * ***** ** ** ***** ***** * ** *
229 : CGTGGGAGAT CCGCATGTTT GAATTTGCCC GACTCCGCTT GCGGGCTTCC GGTGCCGGAA

361 : ACTACTTGTC CTAAGGAGAT TCAGAA-AGC TCGCTCTGAA GCTGCAATGG CGTTTCAGAA
   * * * * * * * * * * ***** ** ***** * * * * * *
289 : TCCAATGATC CGGATGTGA- TAAGAAGAGT TGCGCGGAA GCTGCGGAGA TGTTTAGGCC

420 : TG-AGACTAC GACGGAGGGA TCTAAACTG CGGC---GGA GGCAGAGGAG GCGG-CAGGG
   * * * * * * * * * * * * * * * * * * * * * * * * *
348 : GGTGGATTTA GAAAGTGAA T-TACGGTTT TGCCTTGTGC GGGAGATGAT GTGGATTG

475 : GAGGGGGTGA GGG---AGGG GGAGAGGAGG G--CGGAGGA GCAGAATGGT GGTGTGTTTT
   * *** *** * * * * * * * * * * * * * * * * * *
407 : GTTTTGTTTC GGGTCCGGC TCTGTTTCG GATCGGAGGA GAGGAAT--- --TCTCTTC

530 : ATATGGATGA TGAGGCGCTT TTGGGGATG- CCCAACTTTT TTGA-GAATA TGGCGGAGGG
   ***** *** * * * * * * * * * * * * * * * *
462 : GTATGGATTT GGAGAC---T ACGAAGAAGT CTCAACGACG ATGATGAGAC TCGCGGAGGG

588 : GATGCTTTTG CCGCCGCCG- GAAGTTGGCT GGAA-TCATA A---CGAC-- ----TTTGAC
   * ** ** ***** ** * * * * * * * * * * *
519 : GCCACTAATG TCGCCGCCG GATCGTATAT GGAAGACATG ACTCCTACTA ATGTTTACAC

637 : GGA----- --GTG---G GTGACGTGTC ACTCTGGAGT TTTGACGAGT AA
   *** * * * * * * * * * * * * * *
579 : GGAAGAAGAG ATGTGTTATG AAGATATGTC ATTGTGGAGT TACAGATATT AA

```

+++++

```

Sequence 1 : DREB1E.nuc
Size       : 546

```

Fig. 2-16

0009114

Matching Position : 1 - 546

Sequence 2 : DREB1F.nuc  
 Size : 630  
 Matching Position : 1 - 630

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 69.26 [%]  
 Weight : -221

```

1 : ATGGAACG ACGATATCAC CGTGGCGGAG ATGAAGCCAA AGAAGCGTGC TGGACGGAGG
   *** * ** * * ***** * ***** **** * * ***** *** ****
1 : ATGAATAATG ATGATATTAT TCTGGCGGAG ATGAGGCCTA AGAAGCGTGC GGAAGGAGA

61 : ATTTTCAAGG AGACACGTCA CCCAATCTAC AGAGGCGTGC GCGGTAGGGA CGGCGACAAA
   * ** ***** ***** * *** ***** * **** * * * * *****
61 : GTGTTTAAGG AGACACGTCA CCCAGTTTAC AGAGGCATAA GCGGAGGAA CGGTGACAAA

121 : TGGGTATGCG AAGTCCGTGA ACCGATTCAT CAGCGTCGAG TCTGGCTCGG AACTTATCCG
   ***** * * * * * * * * * * * * * * * * * * * * * * * *
121 : TGGGTCTGCG AAGTCAGAGA ACCGACGCAC CAACGCCGCA TTTGGCTCGG GACTTATCCC

181 : ACGGCAGATA TGGCCGCACG TGCTCAGCAC GTGGCGGTTT TTGCTCTGCG CGGGAGATCC
   ** ***** * * * * * * * * * * * * * * * * * * * * * *
181 : ACAGCAGATA TGGCAGCGCG TGCACACGAC GTGGCGGTTT TAGCTCTGCG TGGGAGATCC

241 : GCGTGTTTGA ATTTCTCCGA TTCTGCTTGG AGGTTGCCGG TGCCGGCATC CACTGATCCG
   ** ***** * * * * * * * * * * * * * * * * * * * * * *
241 : GCATGTTTGA ATTTGCGCGA CTCGCTTGG CGGCTTCCGG TGCCGGAATC CAATGATCCG

301 : GACACGATCA GCGGCACGGC GGCCGAAGCA GCGGAGATGT TCAGGCCGCC GGAGTTTAG-
   ** * * * * * * * * * * * * * * * * * * * * * * * *
301 : GATGTGATAA GAAGAGTTGC GCGGAAGCT GCGGAGATGT TTAGGCCGGT GGA-TTTAGA

360 : TACAGGAATT ACGGTTTTAC CCTCAGC--C AG----- ----TGAGTT T-----
   * ***** * * * * * * * * * * * * * * * * * * * * *
360 : AAGTGAATT ACGGTTTTGC CTTGTGCGGG AGATGATGTG GATTTGGGT TTGGTTCCGG

397 : ----- ----GACA- ----- -CGT-CGGAT -----
   * * * * * * * * * * * * * * * * * * * * *
420 : TTCCGGCTCT GGTTCGGGAT CGGAGGAGAG GAATTCTTCT TCGTATGGAT TTGGAGACTA

409 : -GAAGGAGTC GCTGGAATGA TGATGAGGCT CGCGGAGGAG CCGTTGATGT CGCCGCCAAG
   ***** * * * * * * * * * * * * * * * * * * * * *
480 : CGAAGAATC TCAACGACGA TGATGAGACT CGCGGAGGGG CCACTAATGT CGCCGCCGCG

468 : ATCGTACAT- --TGATATGA ---ATACGAG TGTGTACGTG GACGAAGAAA TGTGTTACGA
   ***** * * * * * * * * * * * * * * * * * * * * *
540 : ATCGTATATG GAAGACATGA CTCCTACTAA TGTTTACAGG GAAGAAGAGA TGTGTTATGA

522 : AGATTTGTCA CTITGGAGTT AC-----TA A
   ***** * * * * * * * * * * * * * * *
600 : AGATATGTCA TTGTGGAGTT ACAGATATTA A
  
```

Fig. 3-1

0046368

[GENETYX-MAC: Maximum Matching]  
Date : 2003.03.03

+++++

Sequence 1 : DREB1A.aa  
Size : 216  
Matching Position : 1 - 216

Sequence 2 : DREB1B.aa  
Size : 214  
Matching Position : 1 - 214

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 85.78 [%]  
Weight : -148

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
*****
1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
***
58 : K WVSEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC D-ATTDHGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
*****
118 : AKDIQKAAAE AALAFQDETC DTTTTHGLD MEETMVEAIY TPEQSEGA FY MDEETMFGMP

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
**
178 : TLLDNMAEGM LLPPPSVQWN HNYDGEG-DG DVSLWSY*

```

+++++

Sequence 1 : DREB1A.aa  
Size : 216  
Matching Position : 1 - 216

Sequence 2 : DREB1C.aa  
Size : 217  
Matching Position : 1 - 217

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 86.70 [%]  
Weight : -154

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
*****
1 : MNSFSAFSEM FGSDYESPV SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
*****

```

Fig. 3-2

0046368

```

61 : KVVCELREP KTRIWLGT QTAEMAARAH DVAAIALRGR SACLNFADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC DATTD-HGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDAFY MDEEAMLGMS

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
    *** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : SLLDNMAEGM LLPSPSVQWN YNFDVEG-DD DVSLWSY*
  
```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 65.04 [%]
Weight            : -56
  
```

```

1 : MNSF-SAF-- SEMFGSDYES SVSSGGDYIP TCLASSCPKKP AGRKKFRETR HPIYRGVRRR
  ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KCLASSCPKKR AGRKKFRETR HPIYRGVRQR

58 : NSGKWVCEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** * * * * * * * * * * * * * * * * * * * * * * * * * *
61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

118 : STCAKDIQKA AEAALAFQD EMCDATTDHG FDMEETLVE- ----AIYTAE QSENAFYMH
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : TTCPEIQKA ASEAAMAFQN ETTTEGSKTA AEAEAAEGEG VREGERRAE QNGGVFYMD

173 : EAMFEMPSLL ANMAEGMLLP LPSVQWNHNNH EVDGDDDDVS LWS--Y
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDG-VGDVS LWSFDE
  
```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 45.87 [%]
Weight            : 32
  
```

Fig. 3-3

0046368

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
  * * * * *
1 : M----- -ENDDI-TVA EMKPKKRAGR RIFKETRHP I YRGVRRRDGD

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC
  * * * * *
40 : K WVCEVREP I HQRVWLGT Y PTADMAARAH DVAVLALRGR SACLNFS DSA WRLPVPASTD

121 : AKDIQKAAAE AALAFQDEMC DATTDHGFD M EETLVEAIYT AEQSENAFY M HDEAMFEMPS
  * * * * *
100 : PD TIRRTAAE AA-----EM- -----FRP PE--FSTGIT VLPSASEFDT SDEGVAGMMM

181 : LLANMAEGML LPLPSVQWNH NHEVD--GDD DDVSLWSY
  * * * * *
145 : RLA-EEPLMS PPRS YIDMNT SVYVDEEMCY EDLSLWSY

```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209

```

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 43.91 [%]
Weight      : 42

```

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
  * * * * *
1 : MN----- -NDDI-ILA EMRPKKRAGR RVFKETRHPV YRGIRRRNGD

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC
  * * * * *
40 : K WVCEVREP T HQRRIWLGT Y PTADMAARAH DVAVLALRGR SACLNFA DSA WRLPVPESND

121 : AKDIQKAAAE AALAF--QDE MCDAT--TDH GFDMEETLVE AIYTAEQSE- -NAFYMHDEA
  * * * * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCA GDDVDLGFSG GSGSGSGSEE RNSSSYGFGD

175 : MFEMPSLLAN MAEGMLLPLP -----SVQW NNNHEVDGDD DDVSLWS--Y
  * * * * *
160 : YEEVSTTMMR LAEGPLMSPP RSYMEDMTPT NVYTEEMCY EDMSLWSYRY

```

+++++

```

Sequence 1      : DREB1B.aa
Size            : 213
Matching Position : 1 - 213

Sequence 2      : DREB1C.aa
Size            : 217
Matching Position : 1 - 217

```



Fig. 3-4

0046368

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+         : 2

Matching     : 86.18 [%]
Weight      : -153

```

```

1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG
   *****
1 : MNSFSAFSEM FGSDYESPV SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

58 : K WVSEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC
    *** * ****
61 : K WVCELREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC

118 : AKDIQKAAAE AALAFQDETC DTTTTNHGLD MEETMVEAIY TPEQSEGAFY MDEETMFGMP
    ** ***** ** **** * ** **** * ** **** * ** **** * **
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDAFY MDEEAMLGMS

178 : TLLDNMAEGM LLPPPSVQWN HNYDGE GGD VSLWSY-
    ***** ** ***** * * *** * *****
181 : SLLDNMAEGM LLPSPSVQWN YNF DVEGDD VSLWSY*

```

+++++

```

Sequence 1      : DREB1B.aa
Size            : 213
Matching Position : 1 - 213

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+         : 2

Matching     : 65.93 [%]
Weight      : -56

```

```

1 : MNSF-SAF-- SEMFGSDYEP QGGD---YCP TLATSCPKKP AGRKKFRETR HPIYRGVRQR
   ** * * * * ** * * ** *****
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR

55 : NSGK WVSEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACL NFA DSAWRLRIPE
    ***** ** ***** ** * **** *****
61 : NSGK WVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACL NFA DSAWRLRIPE

115 : STCAKDIQKA AAEALAFQD ETC DTTTTNH GDMEE---T MVE---AIYTP EQSEGAFYMD
    ** * **** * *** ** * ** *
121 : TTCPK EIQKA ASEAAAFQN ET-TTEGSKT AAEAEAAAGE GVREGERRAE EQNGGVFYMD

170 : EETMFGMPTL LDNMAEGMLL PPSPVQWNHN YDGE GGDV S LWS--Y
    * *** ***** ** * **** * * ****
180 : DEALLGMPNF FENMAEGMLL PPPEVGWNHN -DFDGVGDV S LWSFDE

```

Fig. 3-5

0046368

+++++

Sequence 1 : DREB1B.aa  
 Size : 213  
 Matching Position : 1 - 213

Sequence 2 : DREB1E.aa  
 Size : 181  
 Matching Position : 1 - 181

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 44.95 [%]  
 Weight : 34

1 : MNSFSAFSEM FGSDYEPQGG DYCP TLATSC PKKPAGRKKF RETRHPIYRG VRQRNSGKWV  
 \* \* \* \* \*  
 1 : M-----E NDDITVAEMK PKKRAGRRIF KETRHPIYRG VRRRDGDKWV  
 61 : SEVREPNNKT RIWLGTFQTA EMAARAHDA ALALGRSAC LNFADSAWRL RIPESTCAKD  
 \*\*\*\*\* \* \* \* \* \*  
 43 : CEVREPIHQR RVWLGTYPTA DMAARAHDA VLALGRSAC LNFSDSAWRL PVPASTDPDT  
 121 : IQKAAAEAL AFQDETCDDT TTNHGLDMEE TMVEAIYTP E QSEGA FYMDE ETMFGMPTLL  
 \* \* \* \* \* \* \* \* \* \*  
 103 : IRRTAEEAE MFRPPEFSTG IT-----VLPS ASE---FDTSD EGVAGMMML  
 181 : DNMAEGMLLP PPSVQWNHN---YDGE-GD GDVSLWSY  
 \* \* \* \* \*  
 147 : ---AEEPLMS PPRS YIDMNT SVYVDEEMCY EDLSLWSY

+++++

Sequence 1 : DREB1B.aa  
 Size : 213  
 Matching Position : 1 - 213

Sequence 2 : DREB1F.aa  
 Size : 209  
 Matching Position : 1 - 209

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 43.72 [%]  
 Weight : 43

1 : MNSFSAFSEM FGSDYEPQGG DYCP TLATSC PKKPAGRKKF RETRHPIYRG VRQRNSGKWV  
 \*\* \* \* \* \* \*  
 1 : MN-----NDDIILAEMR PKKRAGRRVF KETRHPIYRG IRRRDGDKWV  
 61 : SEVREPNNKT RIWLGTFQTA EMAARAHDA ALALGRSAC LNFADSAWRL RIPESTCAKD  
 \*\*\*\*\* \* \* \* \* \*  
 43 : CEVREPIHQR RVWLGTYPTA DMAARAHDA VLALGRSAC LNFADSAWRL PVPESNDPDV  
 121 : IQKAAAEAL AF---QDETC DTTTNNHGLD MEETMVEAIY TPEQSE----GAFYMDDE

Fig. 3-6

```

                                -0046368
      *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
103 : IRRVAAEAAE MFRPVDLESG ITVLPCAGDD VDLGFGSGSG SGSGSEERNS SSYGFGDYEE
      *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
172 : TMFGMPTLLD NMAEGMLLP P-----SVQ WNHNYDGE-G DGDVSLWS-- Y
      *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
163 : VSTTMMRL-- --AEGPLMSP PRSYMEDMTP TNVYTEEMC YEDMSLWSYR Y

```

+++++

```

Sequence 1      : DREB1C.aa
Size           : 216
Matching Position : 1 - 216

```

```

Sequence 2      : DREB1D.aa
Size           : 224
Matching Position : 1 - 224

```

Matching Condition.

```

Matches       : -1
Mismatch      : 1
Gaps          : 1
*N+           : 2

Matching      : 65.33 [%]
Weight        : -59

```

```

1 : MNSF-SAF-- SEMFGSDYES PVSSGGDYSP KLATSCPKKP AGRKKFRETR HPIYRGVRQR
  ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSK KLASSCPKKR AGRKKFRETR HPIYRGVRQR

58 : NSGKWVCELR EPNKKTRIWL GTFQTAEMAA RAHDVAAIAL RGRSACLNFA DSAWRLRIPE
    ***** * ***** * * * * * * * * * * * * * * * * * * * *
61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

118 : STCAKEIQKA AAEEALNFQ- ---DEMCHMT TDAHGLDMEE TLVEAIYTPE QSQDAFYMDE
    ** * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : TTCPKIEQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAE QNGGVFYMD

174 : EAMLGMSLL DNMAEGMLLP SPSVQWNYNF DVEGDDVSL WS--Y
    ** * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDGVGDVSL WSFDE

```

+++++

```

Sequence 1      : DREB1C.aa
Size           : 216
Matching Position : 1 - 216

```

```

Sequence 2      : DREB1E.aa
Size           : 181
Matching Position : 1 - 181

```

Matching Condition.

```

Matches       : -1
Mismatch      : 1
Gaps          : 1
*N+           : 2

Matching      : 43.24 [%]
Weight        : 42

```

Fig. 3-7

0046368

```

1 : M-NSFSAFSE MFGSDYESPV SSGDYSPL ATSCPKKAG RKKFRETRHP IYRGVRQRNS
   * * * * *
1 : MENDITVAE M----- ---KPKKRAG RRIFKETRHP IYRGVRRRDG

60 : GKWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPEST
     *****
39 : DKWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFSDS AWRLPVPAST

120 : CAKEIQKAAA EAALNFQDEM CHMTTDAHGL DMEETLVEAI YTPESQDAF YMDEEAMLGM
      * ** * * *
99 : DPDTIRRTAA EAA----EM FRPPEFSTG- ----- ITVLPSASEF DTSDEGVAGM

180 : SLLDNMAEG MLLPSPSVQW NYNFDVEGD- ----DDVSLW SY
      * ** * *
143 : MMRL---AEE PLMSPPRSYI DMNTSVYVDE EMCYEDLSLW SY
  
```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 41.88 [%]
Weight       : 52
  
```

```

1 : MNSFSAFSEM FGSDYESPVS SGGDYSPLA TSCPKKAGR KKFRETRHPI YRGVRQRNSG
   ** * * * *
1 : MN----- ---NDDIILA EMRPKKRAGR RVFKETRHPV YRGIRRRNGD

61 : KWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPESTC
     *****
40 : KWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFSDS AWRLPVPAST

121 : AKEIQKAAA EAALNFQDEM CHMTTDAHGL DMEETLVEAI YTPESQDAF YMDEEAMLGM
      * ** * * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCA GDDVDLGFSG GSGSGSGSEE RNSSSYGFSGD

172 : DEEAMLGMS LLDNMAEGML LPSP----- -SVQWNYNFD VEGDDVSLW S--Y
      * * * *
160 : YEEVSTTMMR L----AEGPL MSPPRS YMED MTPTNVYTEE EMCYEDMSLW SYRY
  
```

+++++

```

Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224
  
```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.

Fig. 3-8

0046368

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N +       : 2

Matching     : 42.17 [%]
Weight      : 50

```

```

1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVQR
  * * * * *
1 : MENDDIT--- ----- -VAEMKPKKR AGRRIFKETR HPIYRGVRRR

```

```

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** ** * ** * ** * ***** ** ***** **
37 : DGDKWVCEVR EPIHQRRVWL GTYPTADMAA RAHDVAVLAL RGRSACLNFS DSAWRLPVPA

```

```

121 : TTCPKETQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAE QNGGVFYMD
    * * * * *
97 : STDPDTIRRT AAEEAEF--- ----- RPPEFSTGIT Y---LPSASE -----FDTSD

```

```

181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHND FDGV----- GDVSLWSFDE
    * ** * * * *
137 : EGVAGM---M MRLAEPLMS PPRS IDMNT SVYVDEEMCY EDLSLWS--Y

```

+++++

```

Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

```

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N +       : 2

Matching     : 42.13 [%]
Weight      : 49

```

```

1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVQR
  ** ----- ** **** * * * * *
1 : MN----- -NDDI ILAEMRPKKR AGRRVFKETR HPVYRGIRRR

```

```

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    * ***** ** **** ** * ** ***** ** ***** **
37 : NGDKWVCEVR EPTHQRRVWL GTYPTADMAA RAHDVAVLAL RGRSACLNFA DSAWRLPVPE

```

```

121 : TTCPKETQKA ASEAAAFQN ETTTEG--SK TAAEAEAAAG EGVREG-ERR AEEQNGGVFY
    * * * * *
97 : SNDPDVIRRV AAEEAEFRP VDLESGITVL PCAGDDVDLG FGSGSGSGSG SEERNSSSYG

```

```

178 : MDDEALLGMP NFFENMAEGM LLPPP----E VGWNHN---- DFDGVGDVSL WSFDE
    * * * * *
157 : FGD--YEEVS TTMMRLAEGP LMSPPRSYME DMTPTNVYTE EEMCYEDMSL WSYRY

```

+++++

Fig. 3-9

0046368

Sequence 1 : DREB1E.aa  
Size : 181  
Matching Position : 1 - 181

Sequence 2 : DREB1F.aa  
Size : 209  
Matching Position : 1 - 209

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 69.38 [%]  
Weight : -71

```

1 : MENDDITVAE MKPKKRAGRR IFKETRHPIY RGVRRRDGDK WVCEVREPIH QRRVWLGTYP
  * **** ** * ***** ***** * ** *** ** ***** * *** *****
1 : MNNDIILAE MRPKKRAGRR VFKETRHPIY RGI RRRNGDK WVCEVREPTH QRRVWLGTYP

61 : TADMAARAHD VAVLALGRS ACLNFSDSAW RLPVPASTDP DTIRRTAAEA AEMFRPPEFS
  ***** ***** ***** ***** * ** * *** ***** *****
61 : TADMAARAHD VAVLALGRS ACLNFADSAW RLPVPESNDP DVIRRVAAEA AEMFRPVDLE

121 : TGITVLP--- -----SASEFD TS-----D EGVAGMMML AEEPLMSPPR
  ***** * ** * * * **** ** *****
121 : SGITVLP CAG DDVDLGFSG SGSGSGSEER NSSYGF GDY EEVSTTMMRL AEGPLMSPPR

157 : SY-IDM-NTS VYVDEEMCYE DLSLWS--Y
  ** ** * ** ***** * **** *
181 : SYMEDMTPTN VYTEEEMCYE DMSLWSYRY
  
```

Fig. 4-1

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+++++

Sequence 1 : DREB2A.nuc  
 Size : 1008  
 Matching Position : 1 - 1008

Sequence 2 : DREB2B.nuc  
 Size : 993  
 Matching Position : 1 - 993

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 63.40 [%]  
 Weight : -222

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
    ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGGCTGTAT ATGAACAAAC CGG----- AACCGAGCA- ----- GCCGAAGAAA

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAG GAGATGGAAA
    ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
43 : AGGAAATCTA GGGCTCGAGC AGGTGGTTTA ACGGTGGCTG ATAGGCTAAA GAAGTGGAAA

121 : GAGTATAACG AGACCGTAGA AG----AAGT TTCTACCAAG AAGA----- ----GGAAA
    ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
103 : GAGTACAACG AGATTGTTGA AGCTTCGGCT GTTAAAGAAG GAGAGAAACC GAAACGCAAA

166 : GTACCTGCGA AAGGGTCGAA GAAGGGTTGT ATGAAAGGTA AAGGAGGACC AGAGAATAGC
    ** ***** * * * * * * * * * * * * * * * * * * * * * * * * * * *
163 : GTTCCTGCGA AAGGGTCGAA GAAAGGTTGT ATGAAAGGTA AAGGAGGACC AGATAATTCT

226 : CGATGTAGTT TCAGAGGAGT TAGGCAAAGG ATTTGGGGTA AATGGGTTGC TGAGATCAGA
    * ***** * * * * * * * * * * * * * * * * * * * * * * * * * * *
223 : CACTGTAGTT TTAGAGGAGT TAGACAAAGG ATTTGGGGTA AATGGGTTGC AGAGATTCCA

286 : GAGCCTAATC GAGGTAGCAG GCTTTGGCTT GGTACTTTCC CTAAGCTGCTA AGAAGCTGCT
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
283 : GAACCGAAAA TAGGAACTAG ACTTTGGCTT GGTACTTTTC CTACCGCGGA AAAAGCTGCT

346 : TCTGCTTATG ATGAGGCTGC TAAAGCTATG TATGGTCCTT TGGCTCGTCT TAATTTCCCT
    ** ***** * * * * * * * * * * * * * * * * * * * * * * * * * * *
343 : TCCGCTTATG ATGAAGCGGC TACCGCTATG TACGGTTCAT TGGCTCGTCT TAATTTCCCT

406 : CGGTCTGATG CGTCTGAGG TACGAGTACC TCAAGTCAGT CTGAGGTGTG TACTGTTGAG
    * ***** * * * * * * * * * * * * * * * * * * * * * * * * * * *
403 : CAGTCTGTTG GGTCTGAGT TACTAGTACG TCTAGTCAAT CTGAGGTGTG TACGGTTGAA

466 : A----- ---CTCCTGG TTGTGTTTAT GTGAAAACAG AGGATCCAGA TTGTGAATCT
    * * * * * * * * * * * * * * * * * * * * * * * * * * * *
463 : AATAAGGCGG TTGTTTGTGG TGATGTTTGT GTGAAGCATG AAGATACTGA TTGTGAATCT

514 : AAACCTTT-- CTCCG---GT GGA--GTGGA GCCGATGTAT TGT----- --CTGGAGAA
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
523 : AATCCATTTA GTCAGATTTT AGATGTTAGA GAAGA-GTCT TGTGGAACCA GGCCGGACAG

558 : TGGTGCGG-A AGAGATGAAG AGAGGTGTT- AAAGC-GGAT AAGCATTGGC TGAGCGAGTT
    * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

Fig. 4-2

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```

582 : TTGCACGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT TACGATTTGC TGTTAGAGTT
615 : TGAACATAAC TATTGGAGTG ATATTCTGAA AGAGAAAGAG AAACAGAAGG AGCAAGGGAT
    *** ** * ***** * * *** * ***** **** **** ** ** *
642 : TGAGCAGCAG TATTGGGGCC AAGTTTTCGA GGAGAAAGAG AAACCGAAGC AGGAA-GAAG
675 : TGTAGAAAC- CTGTCAGCAA CAACAGCAGG ATTCGCTATC TGTTGCAGAC TATGGTTGGC
    * *** ** ***** ** * *** * * * * * **** ** * ** *
701 : AGGAGATACA GCAACAGCAA CAGGAACAGC AACAGC-AAC AGCTGCA-AC -CGGATTTGC
734 : CCAATGATGT GGATCAGAGT --CACTTGA TTCTTCAGAC ATGTTTGATG TCGATGAG-C
    * ** * * * * * * * * * * * * * * * * * * * * *
758 : TTA CTGTTGC AGATTACGGT TGGCCTTGG- -TCTAATGAT ATTGTAAAT- --GATCAGAC
791 : TTCTACGTGA CCTAA--ATG GCGACGATGT GTTTGCAGGC TTAAATCAGG ACCGGTACCC
    **** * ***** * ** *** * * * * * * * * * *
813 : TTCTTGGGAT CCTAATGAGT GCTTTGATAT TAATGAACTC CT---TGGAG ATTTGAA---
849 : GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG GTTTTGATCC
    **** ** * * * * * * * * * * * * * * * * *
867 : --TGAACCTG GTCCCATCA G---AGCCAA GACCAA---- -AACCACGTA AAT----TCT
909 : GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG ATGGTAATGG
    * * * * * * * * * * * * * * * * * * * * *
913 : GGT----- --AGTTATG ATTTGCATCC GCTTCATCTC GAGCCACAGC ATGGTCACG-
969 : ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
    *** * * ***** *** ** * *
962 : --AGTTCAAT GGTTTGAGTT -----CTCT GGATATTTGA
  
```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008
  
```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
#N+          : 2

Matching      : 55.22 [%]
Weight       : -8
  
```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAG- AAACAGAACA CAAATTGATA CATCGAGGAA
    ** ** * ***** * * * * * * * * * *
1 : AT-GCCGT-- ----- CGGAGATTGT TGACAGGAA- -AAG--GAAG TCTCGTGGAA
60 : AAGGAAATCT AGAAGTAGAG GTGACGGTAC TACTGTGGCT GAGAGATTAA AGAGATGGAA
    * ** * * * * * * * * * * * * * * *
44 : CACGAGATGT AGCTG-AGAT TCTAAGGCAA TGGAGAGAGT ---ACAATGA GCAGATTGAG
120 : AGAGTATAAC GAGACCGTAG AAGAAGTTTC TACCAAGAAG AGGAAAG-TA CCTGCGAAAG
    ** ** * * * * * * * * * * * * * *
100 : GCAGAATCTT G-TATCGATG GTGGTG-GTC CAAAATCAAT CCGAAAGCCT CCTCCAAAG
  
```



Fig. 4-3

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```

179 : GGTCAAGAA GGGTTGTATG AAAGGTAAAG GAGGACCAGA GAATAGCCGA TGTAGTTTCA
    * **** * * **** * * **** * * **** * * **** * * **** * * **** * *
158 : GTTCGAGGAA GGGTTGTATG AAAGGTAAAG GTGGACCTGA AAACGGGATT TGTACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
    ***** * * **** * * **** * * **** * * **** * * **** * * **** * *
218 : GAGGAGTTAG ACAGAGGAGA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGACGGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTTCCTTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
    ** *** * **** * * **** * * **** * * **** * * **** * * **** * *
278 : GTGCTAGGTT GTGGCTCGGT ACTTTCCTCA GTTCATATGA AGCTGCATTG GCTTATGACG

359 : AGGCTGCTAA AGCTATGTAT GGTCTTTTGG CTCGTCTTAA T-TTCCC--- -----TC
    **** * * **** * * **** * * **** * * **** * * **** * * **** * *
338 : AGGCGGCCAA AGCTATATAT GGTCACTCTG CCAGACTCAA TCTTCCCAG ATCACAATC

407 : GGTCTGATGC GTCTGAGG-- -TTACGAGTA CCTCAAG-TC AGTCTGAGGT GTGTACTGTT
    * *** * * **** * * **** * * **** * * **** * * **** * * **** * *
398 : GCTCTTCTTC GACTGCTGCC ACTGCCACTG GTGCAGGCTC GGT-TACTGC ATTTTCTGAT

463 : GAGACTCCTG GTTGTGTTCA TGTGAAAACA GAGG---ATC CAGATTGTGA ATCTAAACCC
    ** * * **** * * **** * * **** * * **** * * **** * * **** * *
457 : GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTGT- GTC---AGGT

520 : TTCTCCGGTG GAGTGGAGCC GATG--TATT GTCTGGAGAA TGGTGCAGAA GAGATGAAGA
    * * * * **** * * **** * * **** * * **** * * **** * * **** * *
513 : GAAACTAGAG GATTGTAG-C GATGAATATG TTCTCTTAGA TAGTCTCAG TGTATTAA-A

578 : GAGGTGTAA AGCGGATAAG CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA
    **** * * * * **** * * **** * * **** * * **** * * **** * * **** * *
571 : GAGGAGCTGA A-AGGAAAAG -AGGAAGTGA GGGA---AGA ACATAACT-T GGCTGTTGGT

638 : TTCTGAAAGA GAAAGAGAAA CAGAAGGAGC AAGGGATTGT AGAAACCTG- -TCAGCAACA
    ** *** * * **** * * **** * * **** * * **** * * **** * * **** * *
625 : TTTGGAATTG GACAG-GACT C-GAAAAGG- --GAGACTTT GGATGCTTGG TTGATGGGAA

696 : ACAGCAGGAT TCGCTATCTG TTGCAGACTA TGGT-TGGCC CAA----TG ATGTGGATCA
    * *** * * * **** * * **** * * **** * * **** * * **** * * **** * *
680 : ATGGCAATGA ACAAGAACCA TTG--GAGTT TGGTGTGGAT GAAACGTTTG ATATTAAT--

750 : GAGTCACTTG GATTCTTCA- -GACATGTTT GATGTCGATG AGCTTCTACG TGACCTAAAT
    *** * * * * * **** * * **** * * **** * * **** * * **** * * **** * *
736 : GAGCTATTGG GTATATTAAA CGACAACAAT G-TGTC--TG ---GTC-AAG AGAC---AAT

808 : GGCG-ACGAT GTGTTTGACG GCTTAAATCA GGACCGGTAC CCGGGGAACA GTGTTGCCAA
    * * * * **** * * **** * * **** * * **** * * **** * * **** * *
786 : GCAGTATCAA GTGGATAGAC ACCCAAAT-- -TTCAGTTAC C----AAACG CAGTTTCCAA

867 : CGGTTTCATAC AGGCCCGAGA G--TCAACAA AGTGGTTTTG ATCCGCTACA AAGCCTCAAC
    *** ** * * **** * * **** * * **** * * **** * * **** * * **** * *
839 : --ATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGAT- -TGCTCAACC AGGAGTTGAT

925 : TACGGAATAC CTCCGTTTCA GCTC---GA- --GGGAAAGG ATGGAATGG ATT-----
    ** *** * * * * **** * * **** * * **** * * **** * * **** * * **** * *
895 : TATGGATGTC CTTATGTGCA GCCCAGTGAT ATGGAGAAGT ATGGTATTGA TTTAGACCAT

972 : -----CTTCG ACGA-CTTGA GTT-----AC TTGGATCT-- --GGAGA--- -----
    *** * * * **** * * **** * * **** * * **** * * **** * * **** * *
955 : CGCAGGTTCA ATGATCTTGA CATACAGGAC TTGCATTTTG GAGGAGACAA AGATGTTTCAAT

```

Fig. 4-4

```

1004 : -----AC-T AA
          ** * **
1015 : GGATCTACAT AA

+++++

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

Matching Condition.

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 44.17 [%]
Weight       : 226

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ***
1 : ATG-----TCATCC ATAGAG---

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    * * ***** *** ** ** * **
16 : -----CCA AAAGTA---A TGATGGT---TGGTGCT---AATAA-----GAA-

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG
    * **** * ***** ***** * * *
48 : ---ACAACG A-ACCGT---CCAAAG---C T-----AGT

181 : TCGAAGAAGG GTTGATGAA AGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
    **** * * ***** *** ***** ***** * * * ** * * *
70 : TCGAGGAAAG GTTGATGAG AGGAAAAGGT GGACCGGATA ACGCGTCTTG CACTTACAAA

241 : GGAGTTAGGC AAAGGATTTG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
    ** ***** * * * * * * * * * * * * * * * * * * * *
130 : GGTGTTAGAC AACGCACTTG GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGG-

301 : AGC-AGGCTT TGGCTTGTA CTTTCCCTAC TGCTCAAGAA GCTGCTTCTG CTTATGATGA
    *** * * * * * * * * * * * * * * * * * * * * * *
189 : AGCTCGTCTT TGGCTCGGTA CTTTCGACAC CTCCCGTGAA GCTGCCTTGG CTTATGACTC

360 : GGCTGCT--A AAGCTATGTA TGGTCCTTTG GCTCGTCTTA ATTCCCTCG GTCTGATGCC
    ** *** ***** * * * * * * * * * * * * * * *
249 : CGCAGCTCGT AAGC--TCTA TGGGCTGAG GCTCATCTCA ACCTCCCT--

418 : TCTGAGGTTA CGAGTACCTC AAGTCAGTCT GAGGTGTGTA CTGTTGAGAC TCCTGGTTGT
    ***** ** * * * * * * * * * *
295 : -----GAGT-CCTT AA-----GAAGT---TA C-----CCT-----

478 : GTTCATGTGA AAACAGAGGA TCCAGATTGT GAATCTAAAC CCTTCTCCGG TGGAGTGGAG
    * **** * * * * * * * * *
316 : -----A AAACGGCG-----TCGTCTCCGG CG-----T

538 : CCGATGTATT GTCTGGAGAA TGGTGGCGAA GAGATGAAGA GAGGTGTTAA AGCGGATAAG
    ** * * * * * * * * * * * * * *
338 : CCCA-----GACTACCA AGCAGC-----AACA CCGGTG-----GAAAAAG

```

Fig. 4-5

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```

598 : CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA TTCTGAAAGA GAAAGAGAAA
      ** ** * **** * ***          * * ***   ***   *   ** ****
375 : CA---GC--A GCGACTCTGA -----GT CGCCGTG--- TTC----ATC CAACGAGA--

658 : CAGAAGGAGC AAGGGATTGT AGAAACCTGT CAGCAACAAC AGCAGGATTC GCTATCTGTT
      * * *      ***   ***   **          ** ** ****   * ****
413 : ---TGTATC A-----TGT GGAAGAGTG- -----AC AG-AGGA--- GATATC----

718 : GCAGACTATG GTTGGCCCAA TGATGTGGAT CAGAGTCACT TGGATTCTTC AGACATGTTT
      *** *** ** * ** ***** * * *
447 : ----- --ATG-GGAG CATATAAAGC TGGATT-TGC CG-----GT

778 : GATGTCGATG AGCTTCTACG TGACCTAAAT GGCGACGATG TGTTCGAGG CTAAATCAG
      *** **** * ****          * * ** **   ** *   * * ** ***
477 : AATG--GATG A--TTCT--- --TCAATAT GG---GAAG -----AAG CTACAAT---

838 : GACCGGTACC CGGGGAACAG TGTTGCCAAC GGTTCATACA GGCCCGAGAG TCAACAAAGT
      ** **      ***          ** ***   ***** * **          * * **
513 : -GTCGTTA-- ---GGA---- --TTCCATG GGTTCATGAA GG----- --AGATAAT

898 : GGTTCGATC' CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAGCT CGAGGGAAAG
      * * ** ** * *          ***** *   **** * *
550 : GATATTTCTC GGTT----- --TGATACTTG TATTTCCGGT -----G

958 : GATGGTAATG GATTCTTCGA CGACTTGAG- TTAATTGGAT CTGGAGAACT AA
      * *      *****   * *** * ** *** **
584 : GCT----- -ATTCT---- --AATTGGGA TTCCTTTCAT TCCCCACTTT GA

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

## Matching Condition.

```

Matches       : -1
Mismatch      : 1
Gaps          : 1
*N+           : 2

Matching      : 49.90 [%]
Weight       : 128

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAAT-----T GATACATCGA
    **** *   * ** ***   *** ** ***** * *   * * * ***
1 : ATGGAA---A AGGA--AGAT AACGGATCGA AACAGAGCTC CTCTGCTTCT GTTGTATCCT

56 : GGAAAAGGAA ATCTAGAAGT AGAGGTGACG GTACTACTGT GGCTGAGAGA TTAAAGAGAT
    ** ***      ****   *** *** * *   * ** ** * **   *** *****
56 : CGAGAAG--- ---ACGAAGA AGA-GTG--G TTGAGCCAGT GGAAGCGACG TTACAGAGAT

116 : GGAAAGAGTA TAACGAGACC GTAGAAGAAG TTTCTACCAA GA-AGAGGAA AGTACCTGCG
    **          ***          ***** * * * * **   * *   *** **
107 : GG----- ---GAG--- ---GAAGAAG GAT-TGGCGA GAGCTCGTAG GGTTCAGGCC

175 : AAAGGGTCGA AGAAGGGTTG TATGAAAGGT AAAGGAGGAC CAGAGAATAG CCGATGTAGT

```

Fig. 4-6

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***** **** **** ***** ***** *** ***** **** ***** *** *
148 : AAAGGTTTCA AGAAAGGTTG TATGAGAGGA AAAGGTGGAC CAGAGAATCC TGTGTTGTCG
235 : TTCAGAGGAG TTAGGCAAAG GATTGGGGT AAATGGGTTG CTGAGATCAG AGAGCCTAAT
** ***** * ** * ***** * ***** ***** ***** * ** **
208 : TTTAGAGGTG TTCGACAAAG GGTGTTGGGG AAATGGGTTG CTGAGATACG TGAACC----
295 : CGAGGTAGCA GGCTTTGGCT TGGTACTTTC CCTACTGCTC AAGAAGCTGC TTCTGCTTAT
** ** * * ***** * *** * * ** * ** ** *****
264 : --AGTGAG-- ----TCACCG TGGTGCAAAC TCTAGT-CGT AGTAAACGGC TTTGGCTTGG
355 : GATG-AGGCT GCTAAAGCTA TGTATGGTCC TTTGGCTCGT CTTAATTTCC CTCGGTCTGA
* * *** ** ***** * * * *****
315 : CACGTTTGCT ACTGCAGCT- --GAAGCTGC TTTGGCT--- -----
414 : TGGCTCTGAG GTTACGAGTA CCTCAAGTCA GTCTGAGGTG TGTACTGTTG AGACTCCTGG
* ** * ** * * * ***** ***** *****
349 : TACGACAGA- GCTGCTAGT- ----GTCA ----- TGTAC----- GGAC-CCT--
474 : TTGTGTTTAT GTGAAAACAG AGGATCCAGA TTGTGAATCT AAACCTTCT CCGGTGGAGT
** * ***** ** * ** * ** ***** **
383 : -----AT G----- ----CCAG- --GT-----T AAA---TTTC CCGGAAGATT
534 : GGAGCCGATG TATTGTCTGG AGAATGGTGC GGAAGAGATG AAGA-GAGGT GTTAAAGCGG
* * ** ** ***** * * * ** * ** *
410 : TGGG----- --TG--GG GGAA----- GGAAGA-AGG ACGAGGAGGC GGAAAGTTGC
593 : ATAAGC-ATT GGCTGAGCGA GTTGAACAT AAC---TATT GGAGTGATAT TCTGAAAGAG
* ** *** ** ** * ***** * * ** * ** ***** ***** *
451 : GGAGGCTATT GGTG---GA AACT-AACAA AGCCGGTAAT GCGTGAT-- --TGAACGG
649 : AAAGAGAAAC AGAAGGAGCA AGGGATTGTA GAAACCTGTC AGCAACAACA GCAGGATTCG
** * * ** * * ***** * * ***** *
503 : AAGGTGGAAG AGA-----CT A-----TGTA G----- -TCTACAA-- --TGAAGACG
709 : CTATCTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA
***** * * ***** ** ** * * ** *** ** ** *
539 : CTAT----- ----TGAGC TTGGCC--AT GA-----C A-AG--ACTC AGAATCCT--
769 : GACATGTTTG ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTGCAGGC
*** ** ** ***** * ** ** * * *
574 : ---ATGACTG AT---AATGA AAT---AGT GAAC----- ----CCA-- ----GCAG--
829 : TTAAATCAGG ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT
* ***** ** * ** ***** ** * ** ***** * *
605 : TGAAATCAG- --AGGAA--- -GGTTACAGC TATG--ATCG ATTCAAATTG G-----
889 : CAACAAAGTG GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC
* ** * * ** * ** * ** * * ** *
647 : --ATAACGGA TTGTTG---- --TATAA--- -TGAACCTC- --AAAGCTCC AGTT-ATCAC
949 : GAGGGAAAGG ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
***** * ** * * * ***** * ***** * **
691 : CAGGGA---G GTGG-ATTCG ATTC----AT ATTTTGAGTA TTTGAGAT-- ----TCTAG

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Sequence 1 : DREB2A.nuc  
 Size : 1008  
 Matching Position : 1 - 1008

Fig. 4-7

0010181

Sequence 2 : DREB2F.nuc  
 Size : 834  
 Matching Position : 1 - 834

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 48.48 [%]  
 Weight : 158

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ***                               ****
1 : ATGG-----AGAA-----ATC-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
   ***                               ** * ** *** * *****
12 : -----ATC-----CTC A---ATGAAA CA-ATGGAA-

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TCGGAAAGGG
   33 : -----GAAGGGTCC TGC-----

181 : TCGAAGAAGG GTTGATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
   ***                               ***** ** *** * * * * *
45 : TCG-----GGGTAAAGGC GGTCCACAAA ACGCTCTTTG TCAGTACCGT

241 : GGAGTTAGGC AAAGGATTGG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAA-TCGAGG
   ***** ** * * * * * * * * * * * * * * *
88 : GGAGTCAGGC AAAGGACTTG GGGCAATGG GTGGCTGAGA TCAGAGAGCC CAAGAAGAGG

300 : TAGC-AGGCT TTGGCTTGGT ACTTTCCTTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
   ** ** * * * * * * * * * * * * * * *
148 : --GCAAGACT TTGGCTTGGC TCTTTCGCTA CAGCTGAAGA AGCAGCTATG GCTTATGATG

359 : AGGCTGC--T AAAGCTATGT ATGGTCCTTT GGCTCGTCTT AATTTCCCTC GGTCTGATGC
   ***** * * * * * * * * * * * * * * *
206 : AGGCTGCCTT GAAAC--TCT ATGGGCACGA CGCATACCTC AACTTACCTC -ATCTTCAGC

417 : GTCTGAGGTT ACGAGTACCT CAAGTCAGTC TGAGGTGTGT ACTGT-TGAG ACTCCTGGTT
   * * * * * * * * * * * * * * *
263 : G-----GAAT ACAAG-ACCT ----TC--TC TGAG----TA ACTCTCAGAG GTTC--AAAT

476 : GTGTTTCATGT GAAACAGAG GATCCAGATT GTGAATCTAA ACCCTTCTCC GGTGGAGTG-
   * * * * * * * * * * * * * * *
305 : GGTACCT-- ----TCA-AG GA--AGTTT AT--ATCTAT GTTTCCTTCA TGTGGTATGC

535 : GAGCCGATGT ATTGTCTGGA GAATGGTGCG GAAGAGATGA AGAGAGGTGT-TAAAGCGGAT
   * * * * * * * * * * * * * * *
353 : TAAACG-TGA ATGCTC---A GCCTAGTGTT CACATAATCC AGCAAAGACT AGAAGAACTC

595 : AAGCATTGGC TGAGCGAGTT TGAACATAA- -CTATTGGAG T-GATATTCT GAAAGAGAAA
   *** * * * * * * * * * * * * * * *
409 : AAGAA--AAC TG---GACTT TTATCTCAAT CCTATTCTTC TAGTTCTTCC TCCACCGAAT

652 : GAGAAAC-AG AAGGAGC--A AGGGAT-TGT AGA--AACCT GTCAGCAACA -ACAGCAGGA
   * * * * * * * * * * * * * * *
464 : CAAAACTAA TACTAGCTTT CTTGATGAGA AGACCAGCAA GGGAGAAACA GACAATATG-
```

Fig. 4-8

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```

705 : TTCGCTATCT GTTG--CAG- ----ACTATG GTTGGCCCAA TGA-TGTGGA TC-AGAGTCA
      **** * * * * *      ** * * * * *      *** * * * * *
523 : TTCG-AAGGT GGTGATCAGA AGAAACCAGA GATCGACC-- TGACCGAGTT TCTTCAGCAA

756 : CTTGGATTCT TCAGACATG- -TTTGATGTC GA-----TG AGCT-TCTAC GTGACCTAAA
      ** *** * * * * *      *** * * * * *      ** * * * * *
580 : CTAGGAATCT TGAAGGATGA AATGAAGCA GAACCAAGTG AGGTAGCAGA GTGTCATTCC

807 : TGGCGACGAT -GTGTTTGCA GGCTTAAATC AGGACCGGTA CCCGGGGAAC AGTG-TTGCC
      * * * * *      *** * * * * *      *** * * * * *
640 : CCTCCACCAT GGAACGAGCA AGAAGAAA-C TGGA--AGTC CTTTCAGAAC TGAGAATTTC

865 : AACGGTTCAT A-CAGGCCCG AGAGTCAACA AAGTGGTTTT GATCCGCTAC AAAGC--CTC
      * * * * * * * * * *      *** * * * * *      * * * * *
697 : AGCTG-GGAT ACCCTGATCG AGATGCCAAG AAGTG----- AAACCACAAC TATGCAATTT

922 : AACTACGGAA TACCTCCGTT TCAGCT-CGA GGGAAAGGAT GGTAATGGAT TCTTC---GA
      *** * * * * * * * * *      ***** * * * * *
751 : GACTCCAGCA -ACTTCGG-- -AAGCTATGA TTTTGAGGAT G---ATGTAT CCTTCCCTTC

978 : CGACTTGAGT TACT-TGGAT CTGGAGAACT AA
      * * * * *      **** * * * * *
804 : CATCTGGGAC TACTACGGAA GCTTAG-ATT GA

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches    : 1
Gaps         : 1
*NT+         : 2

Matching      : 47.08 [%]
Weight       : 149

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ****
1 : ATGG-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    : ----- ** * **
    : -----AA G-----AA

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG
     *** *      ***      * *      ***** * *** ** * * *
10 : GAGCA----- --ACC----- --TCCG GCCAAGAA-A CGAA---ACA TGGGGA--GA

181 : TCGAAGAAGG GTTGATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
     ** * * * * * * * * * * * * * * * * * * * * *
46 : TCTAGAAAAG GTTGCATGAA AGGTAAAGGC GGTCCAGAGA ACGCCACGTG TACTTTCCGT

241 : GGAGTTAGGC AAAGGATTTG GGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
     ***** ** *** ** ***** ** ***** ** * ***** ** *

```

Fig. 4-9

0010181

```

106 : GGAGTTAGGC AACGGACTTG GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG
301 : AGCAGGCTTT GGCTTGGTAC TTTCCCTACT GCTCAAGAAG CTGCTTCTGC TTATGATGAG
    * * * * *
166 : ACTCGTCTCT GGCTCGGCAC GTTAAATACC TCGGTCGAGG CCGCCATGCC TTACGATGAA

361 : GCTGCTAAAG CTATGTATGG TCCTTTGGCT CGTCTTAATT TCCCTCGGT- CTGATGCGTC
    ** ***** * **** ** ** ** *** * *
226 : GCCGCTAAGA AACTCTATGG ACACGAGGCT AACTCAA-- ---CTTGGTG CACCCACAAC

420 : TGAGGTTACG AGTACCTCAA GTCAGTCTGA GGTGTGTACT GTTGAGACTC CTGGTTGTGT
    ** **** * * * * *
281 : AACACAACA AGTA---GTA GTGA-ACAGA AACTTGTCTT TTTCTGGCCA CGGGTCGGGT

480 : TCATG----T GAAAACAGAG GATCCAGATT GTGAAT---C TAAACCCT-- TCT---CCGG
    ** * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTGG TCTCGGCCAG

528 : TGGAGTGGAG C-CGATG-TA TTGTCTGGAG A-ATGGTGGC GAAGAGATGA AGAGAGGTGT
    *** * * * * *
397 : GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGA-TGATGA

585 : TAAAGCGGAT AAGC-AT-TG GCTGAGCGAG TTTGAACATA ACTATTGGAG TGATATTCTG
    * * * * *
456 : TCATAGTCAT AATCGATGTT CGTCTTCAAG -TGGTTCGAA TCT-TTGTG -GTTATTACC

643 : AAAGAGAAAG AGAAACAGAA GGAGCAAGGG ATTGTAGA-- ----AACCTG TCA--GCAAC
    ** * **** ** * * *
513 : TAA-ACAAAG TGATTCACAA -GATCAAGAG ACCGTTAATG CTACGACTAG TTATGGCGGT

695 : AACAGCAGGA TTCGCTAT-- ----CTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC
    * * * * *
571 : GAAGGCGGTG GTGGCTCTAC GTTAACGTTT TCGACCAATT TGAACCAAA GAATTTGATG

749 : AG--AGTCAC TTGATTCTT CA---GA--- ----CATGT TTGATGT--- -CGATGAGCT
    ** ** * * * *
631 : AGTCAGAATT ATGGATTATA CAATGGAGCT TGGTCTAGGT TTCTTGTGGG GCAAGAAAAG

792 : TCTACGTGAC CT-AAATGGC GACGATGTGT TTGCAGGCTT AAATCAGGAC CGGTACCCGG
    *** ** * * * *
691 : AAGACGGAAC ATGACGTGTC ATCGTCGTGT GGATCGTCGG ACAACAAGGA GAGTATGTTG

851 : GGAAC-AG-T GTTGCCAACG GTTCATACA- GGCCCGAGAG TCAACAAAGT GGTTTTGATC
    * * * * *
751 : GTTCCTAGTT GCGGCGGAGA GAGGATGCAT AGGCGG-GAG TTGGAAGAGC GAACAGGATA

908 : CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAG-- --CTCGA-GG GAAAGGATGG
    ** * * * *
810 : TTTGGAAATG GATGATCTTT TGGAGATTGA TGATTTAGGT TTGTTGATTG GCAAAAATGG

963 : -----T AATGGATTCT TCGACGACTT --GAGTTACT TGGATCTGGA GAACTAA
    *** * * *
870 : AGATTITCAAG AATTGGTGT GTGAAGAGTT TCAACATCCA TGAATTG-- GTTCTGA
  
```

+++++

Sequence 1 : DREB2A. nuc  
 Size : 1008  
 Matching Position : 1 - 1008

Sequence 2 : DREB2H. nuc

Fig. 4-10

0010181

Size : 534  
 Matching Position : 1 - 534

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 39.41 [%]  
 Weight : 304

```

1 : ATG-GCAGTT TATGATCAGA GTGGAGATAG AACAGAAACA CAAATTGATA CATCGAGGAA
   *** ** * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGCCCAGGA AACG-GAAGT CTCGTG----- ----GAACA CGAGATGTAG CTGAGATTCT

60 : AAGGAAATCT AGA-AGTAGA GGTGACGGTA CTAAGTGGC TGACAGATTA AAGAGATGGA
   ***** ** * * * * * * * * * * * * * * * * * * * * * *
51 : AAGGAAATGG AGAGAGTACA -ATGA--GCA -GACCGAGGC ----AGATTC TTG-CATCGA

119 : AAGAGTATAA CGAGACCGTA GAAGAAGTTT CTACCAAGAA GAGGAAAGTA CCTGCGAAAG
   * * * * * * * * * * * * * * * * * * * * * * * * * * *
102 : TGGTG----- ----GTG GTTCAA----- -AACCAATCC GA--AAGGCT CCTCCAAAC

179 : GGTGGAAGAA GGGTGTATG AAAGGTAAAG GAGGACCAGA GAATAGCCGA TGTAGTTTCA
   * * * * * * * * * * * * * * * * * * * * * * * * * * *
143 : GTTCGAGGAA GGGTGTATG AAAGGTAAAG GTGGACCTGA AAATGGGATT TGTGACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
   ***** ** * * * * * * * * * * * * * * * * * * * * *
203 : CAGGAGTTAG ACAGAGGACA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGGCCGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTCCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
   ** * * * * * * * * * * * * * * * * * * * * * * * * *
263 : GTGCTAAGTT ATGGCTCGGT ACTTCTCTA GTTCATATGA AGCTGCATTG GCTTATGATG

359 : AGGCTGCTAA AGCTATGTAT GGTCTTTGG CTCGTCTTAA TTTCCCTCGG TCTGATGCGT
   ***** * * * * * * * * * * * * * * * * * * * * *
323 : AGGCTTCCAA AGCTAT----- ----TTA- ----CGG TC-----AGT

419 : CTGAGGTTAC GAGTACCTCA AGTCAGTCTG AGGTGTGTAC TGTGAGACT CCTGGTTGTG
   *** * * * * * * * * * * * * * * * * * * * * * *
350 : CTG----- ----CCCG ACTCAATCT- ----TCCAC TGCTGCCAC- ----TGTG

479 : TTCATGTGAA AACAGAGGAT CCAGATTGTG AATCTAAACC CTTCTCCGGT GGAGTGGAGC
   * * * * * * * * * * * * * * * * * * * * *
384 : T----- ----CAGGCT C--GGTT--- ----AC- ----

539 : CGATGTATTG TCTGGAGAAT GGTGCGGAAG AGATGAAGAG AGGTGTTAAA GCGGATAAGC
   ** * * * * * * * * * * * * * * * * * * *
398 : ---TGCATTT TCT----- ----GATGAA-----

599 : ATTGGCTGAG CGAGTTTGAA CATAACTATT GGAGTGATAT TCTGAAAGAG AAAGAGAAAC
   **** * * * * * * * * * * * * * * *
414 : ----TCTGA- --AGTTTG-- ---- --TGCACGTG A-----

659 : AGAAGGAGCA AGGAGTTGTA GAAACCTGTC AGCAACAACA GCAGGATTGCT CTATCTGTTG
   **** * * * * * * * * * *
434 : ----- --GAT----- ----ACAAAT GCA-----

```



Fig. 4-11

0010181

```

719 : CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA GACATGTTTG
      *** * *** **          * * * * *** ** **          ****
447 : -AGA-TCTGG TT----- ---TTGGTC AGA-TCTCT- ---AACTTC- -----

779 : ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTCAGGC TTAAATCAGG
      ***          * *   ** *****          **** **
477 : ---TCG----- ---CAT TTCCAAAATG ----- ---TTAAGTC---

839 : ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG
      ** *          ***   * ***          **
500 : -----CAAT -----AAC- -TGCAT----- ---TG

899 : GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG
      ***          ***          **          ***
514 : GTT----- ---AAG- ----- ---TT----- ---GGG-----

959 : ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
      * ***          ****
525 : -----GCGTT -----ACTAG
  
```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993
  
```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

Matching     : 54.32 [%]
Weight       : 12
  
```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
  ** ** **          *** *   * * * * * * * * * * * * * *
1 : AT-GCCGT-- -----CGG-AGATTG TTGAC-AGGA AAAGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGGA AAGAGTACAA CG---AGATT
   ** * * *   ** ** *** *   * * * * * * * * * * * * * *
43 : ACACGAGAT- -----GTAGC TGAGATTCTA AGGCAATGGA GAGAGTACAA TGAGCAGATT

118 : GTTGAAGCTT CGGCTGTAA AGAAGGAG-- -AGAAACCGA AACGCAAAGT TCCTGCGAAA
   * * * * *   * * * *   * * * *   * * * *   * * * *   * * * *
97 : GAGGCAGAAT CTTGTATCGA TGGTGGTGGT CAAAATCAA TCCGAAAGCC TCCTCCAAA

175 : GGTCGAAGA AAGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
   ** **** ** * * * * * * * * * * * * * * * * * * * * * *
157 : GGTTCGAGGA AGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAACGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCCAGA ACCGAAAATA
   ***** * * * * * * * * * * * * * * * * * * * * * *
217 : AGAGGAGTTA GACAGAGGAG ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGACCGA

295 : GGAAGTAGAC TTTGGCTTGG TACTTTTCCT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT
  
```

Fig. 4-12

```

                                -0010181
277 :  ** **** * ***** ** ***** * * * * ***** * *****
      GGTGCTAGGT TGTGGCTCGG TACTTCTCC AGTTCATATG AAGCTGCATT GGCTTATGAC

355 :  GAAGCGGCTA CCGCTATGTA CGGTTCAATG GCTCGTCTTA A-CTTCCC-- --TCA-----
      ** ***** * ***** ** *** * ** * * * * ***** ***
337 :  GAGGCGGCCA AAGCTATATA TGGTCAGTCT GCCAGACTCA ATCTCCCGA GATCACAAAT

405 :  ----- -GTCTG----- -TT GGGTCTG--- AGTTTACTAG TACGTCTAGT
      * *** * * * * * * * * * * * * * * * * * * * * * * * * *
397 :  CGCTCTTCTT CGACTGCTGC CACTGCCACT GTGTCAGGCT CGGTACTGC ATTTTCTGAT

439 :  CAATCTGAGG TGTGTACGGT TGAAAATAAG GCGGTTGTTT GTGGTGATGT TTGTGTGAAG
      ***** * * * * * * * * * * * * * * * * * * * * * * * * *
457 :  GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTGG TCAGGTGAAA

499 :  CATGAAGATA CTGATTGTGA ATCTAATCCA TT---TAG-- -TCAG---AT TTTAGA----
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *
517 :  CTAGAGGATT GTAGCGATGA ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG

546 :  -TGTTA-GAG AAGA-GTCTT GTG----GAA CCAGGCCGGA CAGTTG--CA CGG--TTGGA
      ** * * * * * * * * * * * * * * * * * * * * * * * * * *
577 :  CTGAAAGGAA AAGAGGAAGT GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGAATTGGA

595 :  CA----TCAA GATATGAATT CTTGCTGAA TTACGATTG CTGTTA---G AGTTTGAGC-
      ** * * * * * * * * * * * * * * * * * * * * * * * * * *
637 :  CAGGACTCGA -AAAGGGAGA CTT---TGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA

647 :  AGCAGTATTG GGGCCAAGTT TTGCAGGAGA AAGAGAAACC GAAGCAGGAA GAAGAGGAGA
      ** * * * * * * * * * * * * * * * * * * * * * * * * * *
693 :  AGAACCATTG GAG-TTTGGT GTGGATGAAA CGTTTGATAT TAATGAGCTA -TTGGGTATA

707 :  TACAGCAACA GCAACAGGAA CAG-CAACAG -CAA--CAGC TGCAACCGGA TTTGCTTACT
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *
751 :  TTAAACGACA ACAATGTGTC TGGTCAAGAG ACAATGCAGT ATCAAGTGGA TAGAC--AC-

763 :  GTTGCAAGATT ACGGTTGGCC TTGGTCTAAT G-ATATTGTA AATGATCAGA CTT-CTTGGG
      ** *** * *** * * * * * * * * * * * * * * * * * * * *
808 :  ---CCAAATT TCAGTT----- -ACCAAAC GCAGTTTCCA AAT--TCTAA CTGCTCGGG

821 :  ATCCTAATGA GTGCTTTGAT ATTAATGAAC TCCTTGGAGA TTTGAATGAA CCTGGTCCCC.
      * * * * * * * * * * * * * * * * * * * * * * * * * * *
856 :  AGCCTCA--A CCCTATGGAG ATTGCTCAA- --CCAGGAG- -TTG-ATTAT GGATGTCTT

881 :  ATCAGAGCCA AGACCAAAAC CACGTA-AAT TCTGGTAGTT ATGATTGCA T--CCGCTTC
      ** * * * * * * * * * * * * * * * * * * * * * * * * * *
908 :  AT--GTGC-- AGCCCAAGTA TATGGAGAAC TATGGTATTG ATTTAGACCA TCGCAGGTTT

938 :  ----ATCTCG AGCCACACGA --TGG--TCA CGAG--TTCA ATGGTTTGAG TTCTCTGGA-
      ***** * * * * * * * * * * * * * * * * * * * * * * *
964 :  AATGATCTTG ACATACAGGA CTTGGATTGTT GGAGGAGACA AAGAT----G TTC-ATGGAT

987 :  -TATTTGA
      ** * *
1019 :  CTACATAA

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

Fig. 4-13

```

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

Matching Condition.

Matches        : -1
Mismatch       : 1
Gaps           : 1
*NT+           : 2

Matching       : 43.12 [%]
Weight         : 231

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
*** *          * * * * * * * * * * * * * * * *
1 : ATGTC-----ATC C---ATAGAG C-----CA AAAGTAA-----

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CGAGATTGTT
* * * * * * * * * * * * * * * * * * * * * *
26 : --TGATGGTT ---GGT-GC TAAT-----AAGAA-----ACAA CGA-ACCGTC

121 : GAAGCTTCGG CTGTTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
* * * * * * * * * * * * * * * * * * * * * *
61 : CAAGCT-----AGT-----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
* * * * * * * * * * * * * * * * * * * * * *
73 : AGGAAAGGTT GTATGAGAGG AAAAGGTGGA CCCGATAACG CGTCTTGCAC TTACAAAGGT

241 : GTTAGACAAA GGATTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA AATAGGAACT
* * * * * * * * * * * * * * * * * * * * * *
133 : GTTAGACAAAC GCACTTGGGG CAAATGGGTC GCTGAGATCC GCGAGCCTAA CCGAGGAGCT

301 : AGACTTTGGC TTGGTACTTT TCCTACCGCG GAAAAAGCTG CTTCCGCTTA TGATGAAGCG
* * * * * * * * * * * * * * * * * * * * * *
193 : CGTCTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CCTTGGCTTA TGACTCCGCA

361 : GCTACCGCTA TGTACGGTTC ATTGGCTCGT CTTAACTTCC CTCAGTCTGT TGGGTCTGAG
*** * * * * * * * * * * * * * * * * * * * * *
253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTC-CT TAAG---AAG

421 : TT-TACTAGT ACGTCTAGTC AATCTGAGGT GTGTACGGTT GAAAAATAAGG CGGTTGTTTG
** *** * * * * * * * * * * * * * * * * * *
309 : TTACCCTAAA ACGGC--GTC -GTCTCCGGC GTCCAGACT --ACACCAAG CAGCAACACC

480 : TGGTGATGTT TGTGTGAAGC ATGAAGATAC TGATTGTGAA TCTAATCCAT -TTAGTCAGA
* ** * * * * * * * * * * * * * * * * * * *
364 : GGTGGAAA-- -----AAGC A-GCAG---- CCACTCTGAG TC---GCCGT GTTCATCCAA

539 : TTTTAGATGT TAGAGAAGAG TCTTGTGGAA CCAGGCCGGA CAGTTGCACG GTTGGACATC
* * * * * * * * * * * * * * * * * * * * *
408 : --CGAGATGT CA-----TCATGTGGAA ----GAGTGA CAG-----AG G--AGATATC

599 : AAGATATGAA TTCTTCGCTG AATTACGATT TGCTGTTAGA GTTTGAGCAG CAGTATTGGG
* * * * * * * * * * * * * * * * * * * * *
447 : ATGGGA-GCA T-----ATA AACGTGGATT TGCCGGTAAT GGATG-----ATTCTT--

659 : GCCAAGTTTT GCAGGAGAAA GAGAAACCGA AGCAGGAAGA AGAGGAGATA CAGCAACAGC
*** * * * * * * * * * * * * * * * * * *
491 : --CAA--TAT G-----GGAAGA-----

```

Fig. 4-14

0010181

```

719 : AACAGGAACA GCAACAGCAA CAGCTGCAAC CGGATTTGCT TACTGTTGCA GATTACGGTT
      **** ***
504 : ----- -AGCTACAA- ----- ---TGTCG-- --TTA-GGAT

779 : GGCCTTGGTC TAATGATATT GTAAATGATC AGACTTCTTG GGATCCTAAT GAGTGCTTTG
      ** *** * **** * * ** * * * **** * *
524 : TTCCATGGGT TCATGA---A GGAGATAATG ATATTTCTCG G----- ----TTTG

839 : ATATTAATGA ACTCCTTGA GATTGAATG AACCTGGTCC CCATCAGAGC CAAGACCAAA
      *** **** *** * **
566 : ATA----- ---CTTG-- TATTT----- ---CCGG-- -----

899 : ACCACGTAAA TTCTGGTAGT TATGATTTGC ATCCGCTTCA TCTCGAGCCA CACGATGGTC
      *** * * * *** * ** * **** * ** *
582 : ----- ---TGGCTAT TCTAATTGGG ATTCCTTTCA T-TC---CC- ----C

959 : ACGAGTTCAA TGGTTTGAGT TCTCTGGATA TTGA
      ** ****
615 : AC----- ----- TTTGA

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 49.22 [%]
Weight       : 140

```

```

1 : ATGG---CTG TATATGAACA AACCGGAACC GAGCAGCCGA AGAAAAGGAA ATCTAGGGCT
   **** * * ** *** * ** *** **** ** * * ** **
1 : ATGGAAGG AAGAT-AACG GATCGAAACA GAGC-TCCTC TGCTTCTG-- TTGTA-TCCT

58 : CGAGCAGGTG GTTTAACGGT GGCTGATAGG CTAAGAAGT GGAAAGAGTA CAACGAGATT
     **** * * * ** ** ** *** * * **** *** * ** **
56 : CGAG-AAGAC GAAGAAGAGT GGTGA---G C-----CAGT GGA----- -AGCGACGTT

118 : GTTGAAGCTT CGGCTGTTAA AGAAGGA--- GAGAAACCGA AACGCAAAGT TCCTGCGAAA
      ** * ** * * **** * * * * * ** * ** * **
99 : ACAGA--GAT GGGAGG---A AGAAGGATTG GCGAGAGC-- -TCGTAGGT TCAAGCCAAA

175 : GGGTCGAAGA AAGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
      ** **** * **** * * ** * * **** * * ** *
151 : GGTTCGAAGA AAGTTGTAT GAGAGGAAA GGTGGACCAG AGAATCCTGT TTGTCGGTTT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCGAGA ACC-----
      ***** * **** * * **** * * **** * * **** *
211 : AGAGGTGTTT GACAAAGGAT TTGGGGGAAA TGGGTTGCTG AGATACGTGA ACCAGTGAGT

288 : -----G AAAA---TAG --GAACATA-- -GACTTTGGC TTGGTACTTT TCCTACCGCG
      * ** * * * * * * **** * * * * *

```

Fig. 4-15

0010181

```

271 : CACCGTGGTG CAAACTCTAG TCGTAGTAAA CGGCTTTGGC TTGGCACGTT TGCTACTGCA

331 : GAAAAAGCTG CTTCCGCTTA TGATGAAGCG GCTACCGCTA TGTACGGTTC ATTGGCTCGT
      * ***** ** *** **** * * ***** * * * *
331 : GCTGAAGCTG CTTTGGCTTA CGACAGAGCT GCTAGTGCA TGTACGGACC CTATGCCAGG

391 : CTTAACTTCC CTCAGTCTGT TGGGTCTGAG TTTACTAGTA CGTCTAGTCA ATCTGAGGTG
      * ** **** * * * ***** * * ** * ** * *
391 : TTAAATTCC CGGAAGAT-T TGGGTGGGGG -----AAGGA -----AG-A A-----

451 : TGACCGTTG AAAATAAGGC GGTGTTTGT GGTGATGTTT GTGTGAAGCA TGAAGATACT
      * *** * .**** * * * *** * * * * *
429 : -GGACG---- -AGGAGGC GG----- -AAAGTT- -----CG GGAGGCTATT

511 : GATTGTGAAT CTAATCCATT TAGTCAGATT TTAGATGTTA GAGAAGAGTC TTGTGGAACC
      * *** *** **** * * * * * ** *** * ** * * *
461 : GGTG-GAAA CTAA--CA-- AAGCCGG-- -TA-ATG-- -----GCGTG AT-TGAAA--

571 : AGGCCGGACA GTTGACCGGT TGGACATCAA GA-TATGAAT TCTTCGCTGA ATTACGATT
      **** * **** ** * **** * *** * * * *
500 : ---CGGA-- -----AGG TGA--AAA GACTATGTAG TCTAC----A ATGAAGA--C

630 : GCTGTTAGAG TTTGAGCAGC AGTATTGGGG CCAAGTTTTG CAGGAGAAAG AGAAACCGAA
      *** **** * * * * * ** * * * * *
538 : GCT----- ATTGAGC--- ----TT--GG CCA----TG -ACAAGACTC AGAATCCTAT

690 : GCAGGAAGAA GAGGAGATAC AGCAACAGCA ACAGGAACAG CAACAGCAAC AGCTGCAACC
      * **** * * * * **** * **** * * *
576 : G----- --ACTGATAA TGAAATAG-- ---TGAAC-- --CCAGCA-- --GTGAAATC

750 : GGATTGCTT ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA
      ** * ** **** * ** *****
612 : AGA----- --GGAAG GTTACAG-- -----CT -----ATGATC-

810 : GACTTCTTGG GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTTGAATGA
      *** * ** * * * * * * * * *
635 : ----- GATTCAAA-- ----TTGGA T-----AA CGGATTGTTG --TATAATGA

870 : ACCTGGTCCC CATCAGAGCC AAGACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTGCA
      **** * * * * * **** *
669 : ACCT----- -----CAAA- -----GC-

930 : TCCGCTTCAT CTCGAGCCAC ACGATGGTCA CGAGTTCAAT GGTGTTGAGTT CTCTGGATAT
      *** ** * * * * * * * * * *
679 : TCCAGTT-AT CACCAGGGA- --GGTGGATT CGA-TTC-AT ATTTGAGTA TTTCAGAT-T

990 : TTGA
      *
732 : CTAG
  
```

+++++

Sequence 1 : DREB2B.nuc  
Size : 993  
Matching Position : 1 - 993

Sequence 2 : DREB2F.nuc  
Size : 834  
Matching Position : 1 - 834

Matching Condition.

Fig. 4-16

0010181

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*NT         : 2

Matching     : 48.46 [%]
Weight       : 138

```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   ****                               *** **   ***   ***
1 : ATGG-----AGAA--TCATC-----CTC--

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CGAGATTGTT
    * * ***   ****
18 : -----A ATGAA-----ACAA-----

121 : GAAGCTTCGG CTGTTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
    **   ** **   * * * * * * * * * *
28 : -----TG-----GA AG-----A AGGGTCCTGC-----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
    *** * * * * * * * * * * * * * * * *
48 : -----GGG TAAAGGCGGT CCACAAAACG CTCTTTGTCA GTACCGTGGA

241 : GTTAGACAAA GGATTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA -AATAGGAAC
    ** ** * * * * * * * * * * * * * * * *
91 : GTCAGGCAAA GGAATTGGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGG-GC

300 : TAGACTTTGG CTGGTACTT TTCCTACCGC GGAAAAAGCT GCTTCGCTT ATGATGAAGC
    * * * * * * * * * * * * * * * * * *
150 : AAGACTTTGG CTGGCTCTT TCGCTACAGC TGAAGAAGCA GCTATGGCTT ATGATGAGGC

360 : GGCTACCGCT ATGTACGGTT CATTGGCTCG TCTTAACCTC CCTCAGTCTG TTGGGTCTGA
    **   * * * *   **   * * * * * * * * * *
210 : TGCCTTGAAG CTCTATGGGC ACGACGCATA CCTCAACTTA CCTCA-TCTT CAGCG-----

420 : GTTACTAGT ACGTCT---A GTCAATCT-- GAGGTGTGTA CGGTTGAAAA TAAGGCGGTT
    * * * * * * * * * * * * * * * * * *
264 : GAATACAAGA CTTTCTCTGA GTAACTCTCA GAGGTTCAAA TGGGT-ACCT TCA--AGGAA

475 : GTTGTGGTG ATGTTGTGT GAAGCATGAA G-ATACTGAT TGTGAAT-CT AATCCATTTA
    **** *   ** * * * *   ****   * * * *   * * * * * *
321 : GTTTAT---- ATCTATGTTT CCTTCATGTG GTATGCTAAA CGTGAATGCT CAGCC---TA

533 : GTCAGATTTT AGATGTTAGA GAAGAGTCTT GTGGAAC-CA GG----CCGG ACAGTT---G
    **   **   * * * *   * * * * * * * * * *
374 : GT----GTTT ACATAATCCA GCAAAGACTA GAAGAACTCA AGAAACTGG ACTTTTATCT

585 : CACGGTTGGA CATCAAGATA TGAATTCTTC GCTGAATTAC GATTGCTGT TAGAGT--TT
    **   *   * * * * *   * * * *   * * * *   * * * *
430 : CAATCCTATT CTTCTAGTTC T---TCCTCC ACCGAATCAA AAATAATAC TAGCTTTCTT

643 : GAGCAGCAGT ATTGGGGCCA AGTTTTCAG GAGAAAGAGA AACCGAAGCA GGAAGAAGAG
    ** ** ** *   * ** **   * * * * * * * * * *
487 : GATGAGAAG- ACCAG---CA AG-----G GAGAAACAGA CA-ATATGTT CGAAG--GTG

703 : GAGATACAGC AACAGCAACA G---GAACAG CAACAGCAAC AGCTGCAACC GGATTGCTT
    * * * * * * * * * *   * * * *   * * * *   * * * *
533 : GTGAT-CAGA AGAAACCAGA GATCGACCTG ACCGAGTTTC TTCAGCAACT AGGAATCTTG

```

Fig. 4-17

0010181

```

760 : ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA GACTTCTTGG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
592 : AAGGATGAAA ATGAAG---- --CAGAACCA AGTGAGGTAG CAGAGTGTCA TTCCCTCCA

820 : GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTTG---AA TGAACCTGG-
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
646 : CCATGGAACG AGCAAGAAGA AACT--GGAA GTCCTTTCAG AACTGAGAAT TTCAGCTGGG

876 : -TCCCC--AT C-AGA-GCCA AG-ACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTGCA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
704 : ATACCCTGAT CGAGATGCCA AGAAGTGAAG CCAC---AAC TATGCAA--T TTGA-CTCCA

930 : TCCGCTTC-- -ATCT-CGAG CCACACGATG --GT---CAC GAGTTCAATG GTTTGAGTTC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
758 : GCAACTTCGG AAGCTATGAT TTTGAGGATG ATGTATCCTT CCCTTCCAT- CTGGGACTAC

981 : TCTGGA---- TA-TTTGA
      * * * * * * * * * *
817 : TACGGAAGCT TAGATTGA
  
```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 48.32 [%]
Weight            : 163
  
```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCG-
    **** * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGGAAGAAG AGCAAC-CTC CGG--CCAAG AAACGAAACA TGGGGAGATC TAGAAAAGGT

60 : AGCAGGTGGT TTAACGGTGG --CTGATA-- GGCTAAAGAA -----GTGG AAAGAGTACA
    *** * * * * * * * * * * * * * * * * * * * * * * * * * *
58 : TGCATGAAAG GTAAAGGCGG TCCAGAGAAC GCCACGTGTA CTTTCCGTGG AGTTAG-GCA

110 : ACGAGATTGT TGAAGCTTCG GCTGTTAAAG A-AGGAGAGA AACCGAAACG CAAAGTTCCT
    *** * * * * * * * * * * * * * * * * * * * * * * * * * *
117 : ACGGACTTGG GGTAAT--G GGTGGCTGAG ATCCGTGAG- --CCTAACCG --TGGGACTC

169 : GCGAAAGGGT CGAAGAAAGG TTGTATGAAG GGTAAAGGAG GACCAGATAA TTCTCACTGT
    * * * * * * * * * * * * * * * * * * * * * * * * * * * *
170 : GTCTCTGGCT CG--GCACGT TTAATACCTC GGT---CGAG GCCGCCATGG CTTACGATGA

229 : AG--TTTTAG AGGAGTTA-- GACAAAGGAT TTGGGGTAAA TGGGTTCGAG AGA-TTCGAG
    ** * * * * * * * * * * * * * * * * * * * * * * * * * *
225 : AGCCGCTAAG AAACCTCTATG GACACGAGGC TAAACTCAAC TTGG-TGCAC CCACAACAAC

284 : AACCGAAAT AGGAACTAGA CTTTGGCTTG GTACTTTTCC TACCGCGGAA AAAGCTGCTT
    *** * * * * * * * * * * * * * * * * * * * * * * * * * *
284 : AACACAAGT A-GTAGTGAA CAGAAACTT- GTCTTTTCTT GGCCACGG-G TCGGTTCTT
  
```

Fig. 4-18

0010181

```

344 : CCGCTTATGA TGAAGCGGCT ACCGCTATGT ACGGTTTCATT GGCTCG-TCT TAAC TTCCT
      ***** * * * * * * * * * * * * * * * * * * * * * *
341 : GGGCTTATAA T-AAGAAGCT --CGATAT-- --GGTTCATG GGTGGACCT TGGTCTCGGC

403 : CAGTC-TGTT GGGTCTGAGT TTA CTAGTAC GTCTAGTCAA TCTGAGGTGT GTACGGTTGA
      *** * * * * * * * * * * * * * * * * * * * * * *
394 : CAGGCAAGTT GTTCACGAGG TT-CTTGCTC AGAGAG---A TC-GAGTTTT CTAC--AAGA

462 : AAATAAGGCG GTTGT TTGTG GT-GATGTTT GT-GTGAAGC ATGAAGATAC --TGATTGTG
      * * * * * * * * * * * * * * * * * * * * * * *
447 : AGATGATGAT CATAGTCATA ATCGATGTTG GTCTTCAAGT GGTTCGAATC TTTGTGTTGTT

518 : A--ATCTAAT C-CATTTAGT CAGATTTTGTG ATGTTAGAGA AGAGTCTTG- TGGAACCAGG
      * * * * * * * * * * * * * * * * * * * * * * *
507 : ATTACCTAAA CAAAGTGATT CACA----AG AT-CAAGAGA CCGTTAATGC TACGACTAGT

574 : CCGGACAGTT GCA--CGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT T-----
      * * * * * * * * * * * * * * * * * * * * * * *
562 : TATGGC-GGT GAAGGCGGTG GTGGCTCTAC GT-TAACGTT TTCGACCAAT TTGAAACCAA

623 : ACGATTTGCT G-----T TAGAGTTTGA GCAGCAGTAT TGGGGCCAAG TTT-TGCAGG
      * * * * * * * * * * * * * * * * * * * * * * *
620 : AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC TTGGTCTAGG TTTCTTGTGG

674 : AGAAAGAGAA ACCGAAGCAG GAAGAAGAGG AGATACAGCA ACAGCAACAG GAACAGC-AA
      * * * * * * * * * * * * * * * * * * * * * * *
680 : GGCAAGA-AA A--GAAGACG GAACATGACG TG-----TCA TCGTCGTGTG GATCGTCGGA

733 : CAGCAACAGC TGCAACCGGA TTTGCTTACT GTTGACAGT ACGGTTGGCC TTGGTCTAAT
      * * * * * * * * * * * * * * * * * * * * * * *
732 : CAACAAGGAG AGTATGTTG- GTTCCTAGT GCGGCGGAGA GAGGAT-GCA TAGGCC----

793 : GATATTGTAA ATGATCAGAC TTCTTGGGAT CCTAATGAGT GCTTTGATAT TAATGAAGTC
      * * * * * * * * * * * * * * * * * * * * * * *
786 : GGAGTTGGAA --GAGCGAAC -----AGGAT ----AT---- --TTGGAAT GGATGATCT-

853 : CTTGGAGATT TGAATGAACC TGGTCCCAT CAGAGCCAAG ACCAAAACCA CGTAAATCT
      ***** * * * * * * * * * * * * * * * * * * *
828 : TTTGGAGATT --GATGATT AGGT-----T TGTG--ATT GGCAAAA--A TGGAGATT--

913 : GGTAGTTATG ATTTGCATCC GCTTCATCTC GAGCCACAGC ATGGTCACGA GTTCAATGGT
      * * * * * * * * * * * * * * * * * * * * * * *
875 : -----TCAAG AATTG----- ----GTGTT GTG-----AAG A--GTTTCAA CATCCATGGA

973 : TTGAGTTCTC TGGATATTG A
      * * * * * * * * *
914 : ATTGGTTC-- -----TG A

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

Matches : -1



Fig. 4-19

0010181

```

Mismatches      :      1
Gaps            :      1
*N+             :      2

Matching        :    39.24 [%]
Weight          :    295

```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   **                                     *** * ** * * ** * * * *
1 : AT----- --GCCCAGGA AACGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CG---AGATT
   * * * * * ** ** * * * * * * * * * * * * * * * * * * *
28 : ACACGAGAT- ----GTAGC TGAGATTCTA AGGAAATGGA GAGAGTACAA TGAGCAGACC

118 : GTTGAAGCTT C-GGC--TGT TAAAGAAGGA GAGAAACCGA AACGCAAAGT TCCTGCGAAA
   * * * * * * * * * * * * * * * * * * * * * * * * *
82 : GAGGCAGATT CTGTCATCGA TGGTGGTGGT TCAAAACCAA TCCGAAAGGC TCCTCCAAAA

175 : GGGTCAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
   * * * * * * * * * * * * * * * * * * * * * * * * *
142 : CGTTCGAGGA AGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAATGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCGAGA ACCGAAAATA
   * * * * * * * * * * * * * * * * * * * * * * * * *
202 : ACAGGAGTTA GACAGAGGAC ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGGCCGA

295 : GGAAGTAGAC TTTGGCTTGG TACTTTTCTT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT
   ** *** * * * * * * * * * * * * * * * * * * * * *
262 : GGTGCTAAGT TATGGCTCGG TACTTTCTCT AGTTCATATG AAGCTGCATT GGCTTATGAT

355 : GAAGCGGCTA CCGCTATGTA CGGTTCAATTG GTCGCTCTTA ACTTCCCTCA GTCTGTTGGG
   ** ** * * * * * * * * * * * * * * * * * * * * *
322 : GAGGCTTCCA AAGCTATTTA CGG----- --TCA GTCTG-----

415 : TCTGAGTTTA CTAGTACGTC TAGTCAATCT GAGGTGTGTA CGGTTGAAAA TAAGGCGGTT
   * * * * * * * * * * * * * * * * * * * * * *
353 : -----CCC GACTCAATCT -----TC C-----

475 : GTTTGTGGTG ATGTTTGTGT GAAGCATGAA GATACTGATT GTGAATCTAA TCCATTTAGT
   * * * * * * * * * * * * * * * * * * * * * *
369 : -----ACTG-----CT-- GCCACTGTGT

535 : CAGATTTTAG ATGTTAGAGA AGAGTCTTGT GGAACCAGGC CGGACAGTTG CACGGTTGGA
   ***                                     * * * * * *
385 : CAG----- --G CTCGGTT--A

595 : CATCAAGATA TGAATTCCTC GCTGAATTAC GATTGCTGT TAGAGTTTGA GCAGCAGTAT
   * * * * * * * * * * * * * * * * * * * * *
397 : C-----TGCATTTTCT GATGAAT--- --CTG- --AAGTTTG-

655 : TGGGGCCAAG TTTTGCAGGA GAAAGAGAAA CCGAAGCAGG AAGAAGAGGA GATACAGCAA
   * * * * * * * * * * * * * * * * * * * *
425 : -----TGCACGT GA----- --G GATACA-----

715 : CAGCAACAGG AACAGCAACA GCAACAGCTG CAACCGGATT TGCTTACTGT TGCAGATTAC
   * * * * * * * * * * * * * * * * *
441 : -----AA---TG CAA---GAT- -----CT-

775 : GGTGGCCCTT GGTCTAATGA TATTGTAAAT GATCAGACTT CTTGGGATCC TAATGAGTGC

```

Fig. 4-20

-0010181

```

453 : **** ** **          ***** * ** * *** *
      GGT---TT GG----- --TCAGA--T CT-----C TAA-----C

835 : TTTGATATTA ATGAACCTCT TGGAGATTG AATGAACCTG GTCCCCATCA GAGCCAAGAC
      **          ***      ****          *
474 : TT-----CTC-- --GCATT-- --C

895 : CAAAACCACG TAAATTCTGG TAGTTATGAT TTGCATCCGC TTCATCTCGA GCCACACGAT
      *****          **** * * ** * * ***
486 : CAAA----- --TGTTAAG-- -TCCAATAAC TGCAT-----T

955 : GGTACGAGT TCAATGGTTT GAGTTCTCTG GATATTTGA
      *** * ***      *** * **      ** *
513 : GGTTA--AGT ----TGG--G GCGT----- --TACTAG-
  
```

+++++

Sequence 1 : DREB2C.nuc  
 Size : 1026  
 Matching Position : 1 - 1026

Sequence 2 : DREB2D.nuc  
 Size : 621  
 Matching Position : 1 - 621

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

Matching     : 43.40 [%]
Weight      : 252
  
```

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   *** * **          **          ***
1 : ATGTCATC----- --CA----- --TAG-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
     ** * *      * * ** ****          ** * ****
14 : -----AGCC A-----AAA GT--AATG-- ----- --ATGGTTGGT

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAA--AAGGT TCGAGGAAGG GTTGTATGAA
     * * * * ** *** ** ** * * **** ** ***** * *****
37 : GCTAAT--AAG AAACAA--CG AA----CCGT CCAAGCTAGT TCGAGGAAAG GTTGTATGAG

180 : AGGTAAAGGT GGACCTGAAA ACGGGATTG TGAATATAGA GGAGTTAGAC AGAGGAGATG
     *** ***** ** * *** * ***      ** * * ** ***** * * * **
90 : AGGAAAAGGT GGACCCGATA ACGCGTCTTG CACTTACAAA GGTGTTAGAC AACGCACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGTTGT GGCTCGGTAC
     *** ***** ** ***** **** ***** ** ***** ** * * * *****
150 : GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGGA GCTCGTCTT GGCTCGGTAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGG--CCAA AGCTATATAT
     *** ** ** ***** ***** ***** ** * * * *****
210 : CTTGACACCC TCCCGTGAAG CTGCCTTGGC TTATGACTCC GCAGCTCGTA AGCTCTATGG

358 : G-GTCAGTCT GCCAGACTCA ATCTTCCCGA GATCACAAAT CGCTCTTCTT CGACTGCTGC
     * * ** ** ** ***** * ** ** * *          * ***      * * *
  
```

Fig. 4-21

0010181

```

270 : GCCTGAGGCT --CA-TCTCA ACCTCCCTGA G-----TCCTT AAGAAGTTAC
417 : CACTGCCACT GTGTCAGGCT CGGTTACTGC ATTTTCTGAT GAATCTGAAG TTTGTGCACG
    * ** ** * *** * ** * **
313 : C-CTAAACG GCGTC-GTCT C----CGGC -----GTCC---
477 : TGAGGATACA AATGCAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GTAGCGATGA
    ** **** **** *** * **** ** * ** * * ****
340 : -CAGACTACA ---CCAAG-- CAG---CAAC ACCGGTGGAA --AAAGCA-- GCAGCGA---
537 : ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG CTGAAAGGAA AAGAGGAAGT
    *** * ** * * * * * * * * * * * * * *
384 : -----CTC TGAG-----T CGCCGTG--T TCA-----TCCAACGA- ----GATGT
597 : GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGGAATTGGA CAGGACTCGA AAAGGGAGAC
    *** * * * * * * * * * * * * *
416 : -----CATCA-----TG TGGAA-----GAGT-GA CAGAGGAGA-
657 : TTTGGATGCT TGGTTGATGG GAAATGGCAA TGAACAAGAA CCATTGGAGT TTGGTGTGGA
    * **** ** * * * * * * * *
443 : -----TATCATGG GA-----GCATATAAA C-----GTGGA
717 : TGAACGTTT GATATTAATG AGCTATTGGG TATATTAAAC GACAACAATG TGTCTGGTCA
    *** * * * * * * * * * * * *
468 : -----TTT GCCGGTAATG -----GATG ATTCT--TCA
777 : AGAGACAATG CAGTATCAAG TGGATAGACA CCCAAATTTC AGTTACCAAA CGCAGTTTCC
    * ** *** ** * * * * * * * *
493 : A-----TA-----TGGGAAGAAG CTACAATGTC -GTTA-----GGA-TTTCC
837 : AAATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGATT GCTCAACCAG GAGTTGATTA
    ** * ** *** * ** ** * * * * *
528 : --ATGGGTTT ATG--AAGGA G-----A TAATGATATT TCTC-----GGTTTGATAC
897 : TGGATGTCCT TATGTGCAGC CCAGTGATAT GGAGAACTAT GGTATTGATT TAGACCATCG
    * ** *** * ** *** **** * * * *
570 : T--TG----TATTT-----CCGGTG----GCTAT TCTA--ATT GGA-----
957 : CAGGTTCAAT GATCTTGACA TACAGGACTT GGATTTTGGG GGAGACAAAG ATGTTTCATGG
    *** *** ** * * * *
600 : ----TTC---CTT-TCA TTCCCCACTT -----
1017 : ATCTACATAA
    * *
619 : -----TGA

```

+++++

Sequence 1 : DREB2C.nuc  
 Size : 1026  
 Matching Position : 1 - 1026

Sequence 2 : DREB2E.nuc  
 Size : 735  
 Matching Position : 1 - 735

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2

Fig. 4-22

Matching : 47.50 [%]  
Weight : 184

0010181

```

1 : ATGCCGTCGG -AGATTGTTG ACAGGAAAAG GAAGTCTCGT GGAACACGAG ATGTAGCTGA
   *** ** **** * * * * * ** *** * * **** *
1 : ATGGAAAAGG AAGATAACGG ATCGAAACAG --AG-CTCCT -CTGCTTCTG TTGTATCCTC

60 : GATTCTAAGG CAATGGAGAG AGTACAATGA GCAGATTGAG GCAGAATCTT GTATCGATGG
   ** *** * * * **** * *** ** * ** * ** * ****
57 : GA--GAAGA CGAAGAAGAG TG--GTTGA GCCAGTGGAA GC--GACGTT ACAGAGATG-

120 : TGGTGGTCCA A--AAT---- -CAATCCGAA AGCCTCCTCC AAAAGGTTTCG AGGAAGGGTT
   ** ** * * * * * * ** * * ** * **** * ** * ****
108 : -GGAGGAAGA AGGATTGGCG AGAGCTCGTA GGGTTCAAGC CAAAGGTTTCG AAGAAAGGTT

173 : GTATGAAAGG TAAAGGTGGA CCTGAAAACG GGATTTGTGA CTATAGAGGA GTTAGACAGA
   ***** ** **** * * * * * **** * **** * **** *
167 : GTATGAGAGG AAAAGGTGGA CCAGAGAATC CTGTTTGTGC GTTTAGAGGT GTTCGACAAA

233 : GGAGATGGGG TAAATGGGTT GCTGAGATCC GTGAGCCAGA CGGAGGTGCT AGGTTGTGGC
   ** ***** **** * **** * **** * **** *
227 : GGGTTTGGGG GAAATGGGTT GCTGAGATAC GTGAACCAG- -TGAGTCAC- -----C

293 : TCGGTACTTT CTCCAGTTCA TATGAAGCTG CATTGGCTTA TGACGAGGCG GCCAAAGCTA
   *** * ** * * * * * * * * * * * * * *
275 : GTGGTGCAAA CTCTAG-TCG TAGTAAACGG CTTTGGCTT- -----G GC-----A

353 : TATATGGTCA GTCTGCCAGA CTCAATCTTC CCGAGATCAC AAATCGCTCT TCTTCGACTG
   * * * * ** * * * * * * * * * * * * * *
317 : CGTTTGCT-- -ACTG-CAG- CTGAAGCTGC ----- -TTTGGCT-- -TACGACAG

413 : CTGCCACTGC CACTGTGTCA GGCTCGGTTA CTGCATTTTC TGATGAATCT GAAGTTTGTG
   **** * **** * * * * * * * * * * * * *
357 : ----AGCTGC TA--GTGTC TGTACGG--A C--CCTATGC ----CAGGT TAAATT--

473 : CACGTGAGGA TACAAATGCA AGTTCAGGT TTGGTCAGGT GAAACTAGAG GATTGTAGCG
   * * * * * * * * * * * * * * * * * *
399 : CCCG-GAAGA -----T TTG----GGT G-----GGG GA----AG-G

533 : ATGAATATGT TCTCTTAGAT AGTTCTCAGT GTATTAAGA GGAGCTGAAA GGAAAAGAGG
   * *** * * * * * * * * * * * * *
424 : AAGAA----- -GGACGA GGAGGCG----- -GA

593 : AAGTGAGGGA AGAACATAAC TTGGCTGTTG GTTTTGAAT TGGACAGGAC TCGAAAAGGG
   **** **** * * * * * * * * * * * *
444 : AAGTTCGGGA ----- --GGCTATTG G--TTGGA-- -----AC T---AACAA

653 : AGACTTTGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA AGAACCATTG GAGTTTGGTG
   ** * * * * * * * * * * * * * * * *
477 : AGCCGGTAAT GCGGTGATTG AAACGGAA-G G--TGGAAG AGA--CTATG TAGTCT----

713 : TGGATGAAAC GTTTGATATT AATGAGCTAT TGGGTATATT AAACGACAAC AATGTGTCTG
   ***** ** * * **** * *** ** ***** * * *
527 : ACAATGAA-- ----GACGCT ATTGAGC--T TGGCCAT--- ----GACAAG ACTCAGAATC

773 : GTCAAGA--G ACAATGCAGT ATCAAGTGA TAGACACCCA AATTTCAGTT ACCAAACGCA
   * * * * * * * * * * * * * * * *
572 : CT-ATGACTG ATAATGAA-- AT--AGTG-- ----AACCCA GCAGT--GAA ATCAGAGGAA

```

Fig. 4-23

```

                                -0010181
831 : GTTTCCAAAT TCTAACTTGC TCGGGAGCCT CAACCCTATG GAGATTGCTC AACCAGGAGT
    * ** *      *** ** ***          ** * ****   *** **
619 : GGTTACA--- GCTA---TGA TCG----- -----ATT CAAATTGGAT AACGGATTGT

891 : TG-ATTATGG ATGTCCTTAT GTGCAGC-CC AGTGATATGG AGAACTATGG TATTGATTTA
    ** ** *** *   *** *      *** ** ***   ***   ** * **   ** **
659 : TGTATAATGA A---CCTCA- ---AAGCTCC AGT--TAT-- --CACCAGGG AGGTGGATTG

949 : GACCATCGCA GGTTCATGA TCTTGACATA CAGGACTTGG ATTTTGGAGG AGACAAAGAT
    **          **** * * ****          * ****          ****
706 : GA----- --TTCA--TA TTTTGA----- -----GT ATTT----- ----CAGAT

1009 : GTTCATGGAT CTACATAA
        * *   **
731 : -----T C---TAG

++++++

Sequence 1          : DREB2C.nuc
Size                : 1026
Matching Position   : 1 - 1026

Sequence 2          : DREB2F.nuc
Size                : 834
Matching Position   : 1 - 834

Matching Condition.

Matches             : -1
Mismatch            : 1
Gaps                : 1
*N+                 : 2

Matching            : 48.77 [%]
Weight              : 150

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
    **      ** ***          ** **
1 : AT-----GG AGA----- AA---TC---

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
    ** ** * **** *      ***** ** ****
12 : ATCCT---C AATGAA--- --ACAAT--- -----GG AAGAA-----

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAAGGTT CGAGGAAGGG TTGTATGAAA
    ***          *** ** *          **
36 : --GGGT--- -----CCTGCT C-----GG -----

181 : GGTAAGGTTG GACCTGAAAA CGGGATTGTG GACTATAGAG GAGTTAGACA GAGGAGATGG
    ***** * * ** **** **   ***** * ** * * **** ** **   **** **
49 : GGTAAGGCGG GTCCACAAAA CGCTCTTTGT CAGTACCGTG GAGTCAGGCA AAGGACTTGG

241 : GGTAATGGG TTGCTGAGAT CCGTGAGCC- -AGACGGAGG TGCTAGGTTG TGGCTCGGTA
    ** ***** * ***** * * ***** *** **** ** ** * ***** **
109 : GGCAATGGG TGGCTGAGAT CAGAGAGCCC AAGA-AGAGG -GCAAGACTT TGGCTTGGCT

299 : CTTTCTCCAG TTCATATGAA GCTGCATTGG CTTATGACGA GGCGGCCAAA GCTATATATG
    ***** * *   * *** ** **   ***** ** *** ****   * ****
167 : CTTTCGCTAC AGCTGAAGAA GCAGCTATGG CTTATGATGA GGCTGCCTTG AAACCTCTATG

359 : GTCAGTCTGC CAGACTCAAT CTTCCCGAGA TCACAAATCG CTCTTCTTC- GACTGCTGCC
    * ** **      ***** *** **   ***          ***** * ** * *
227 : GGCACGAGCG ATACCTCAA- CTTACC---- TCA----- -TCTTCAGCG GAATAC-AAG

```

Fig. 4-24

0010181

```

418 : ACTGCCACTG TGTCAAGCTC GGTTACTGCA TTTTCTGATG AATCTGAAGT TTGTGCACGT
    ** * *** ** * *** *      *   *** *** * * * * *
273 : ACCTTCTCTG AGTAACTCTC AG-----A GGTTCAAATG GGT---ACCT TCAAGGAAGT

478 : GAGGATACAA ATG-CAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GT-AGCGATG
    ***   ***   ** ** * *** * * * *** * * * * *
323 : --TTATATCT ATGTTTCCTT CA---TGTGG T-ATGCTAAA C--GTGAATG CTCAGCCTAG

536 : AATATGTTCT CTTAGATAGT TCTCAGTGTA TTAAGAGGA GCTGAAAGGA AAAGAGGAAG
    ***** * *** *   *** *   *** ** * * * * *
375 : ----TGTC- ---ACATAAT --CCAGCAAA GACTAGAAGA ACTCAA--GA AAATGGACT

596 : TGAGGGAAGA ACATAACTTG GCTGTTGGTT TTGGAATTGG ACAGGACTCG AAAAGGGAGA
    *   *   ** **   ** * *** *   *   ** ** ** * *
423 : T----TTATC TCAATCCTAT TCTTCTAGTT CT--TCCTCC AC-CGAATCA AAAACTAATA

656 : CTTTGGATGC TTGGTTGATG GGA--AATGG CAATG----A ACA-AGAA-C CATTGGAGTT
    **   ** ** * * * * * ** * * * * * * * * * *
476 : CT-----AGC TTTCTTGATG AGAAGACCAG CAAGGGAGAA ACAGACAATA TGTTCAAGG

708 : TGGTG--TGG ATGAAACGTT TGATATTAAT GAGCTATTGG GTATATTAAC CGACAACAAT
    ***** * * * * *   *** *   ** *   *   ** * *
531 : TGGTGATCAG AAGAAACCAG AGATCGACCT GACC----GA GTTTCCTT--- CAGCAACTAG

766 : GTGTCTGGTC AAGA-GACAA T---GCAGTA TCAAGTGGAT AGACACCCAA ATTTCAAGTTA
    * *** *   * * * * * *   * * * * *   ** * * *
584 : GAATCTTG-A AGGATGAAAA TGAAGCAGAA CCAAGTG--- AGGTAGCAGA GTGTCA-TTC

822 : CCAAACGCAG TTTCCAAATT CTAAGTTGCT CGGGAGCCTC AACCCATATG AGATTGCTCA
    **   ***** *   *** **   * * *   ** *   *
639 : CC----- -CTCCACCAT GGAACGAGC- AAGAAG---- AAAGTGAAG TCCTTCAGA

882 : AC-CAGGAGT TGATTATGGA TGTCTTAT- GTGCAGCC-- -CAGTGATAT GGAGAACTAT
    ** ** * * *   *** *   *** **   * * *   ***** *
685 : ACTGAGAATT TCAGCTGGGA TACCCTGATC GAGATGCCAA GAAGTGA-AA CCACAACCTAT

937 : GGTA-TTGA- TTTAG-ACCA TCGCAGGTTT AATGATCTTG A-CATACAGG A--CTTGGAT
    * * * * * * * * *   * * *   * * *   * * *   *
744 : GCAATTTGAC TCCAGCAACT TCGGAAG--C TATGATTTTG AGGATGATGT ATCCTTCCCT

991 : TTTGGAGGAG ACAAAGATGT TCATGGATCT ACATAA
    *   * * * * *   * * *   * * *
802 : TCCATCTGGG ACTACTACG- -GAAGCTTAG A-TTGA

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 48.42 [%]

```

Fig. 4-25

Weight : 130

0010181

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   **          **** * ***          ***
1 : AT----- --GGAA---G AAG----- --AGC-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
   * ** *** *   ***   ** **          **          ****
14 : AACCTCCGGC CA-----AGA ---AACGA- ----- --AA----- --CATGG-

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAGGTT CGAGGAAGGG TTGTATGAAA
   **          * * * * * * * * * *
41 : --GG----- ----- --AGAT CTAGAAAAGG TTGCATGAAA

181 : GGTAAAGGTG GACCTGAAAA CGGGATTTGT GACTAT-AGA GGAGTTAGAC AGAGGAGATG
   ***** * * * * * * * * * * * * * * * * * * * * *
67 : GGTAAAGGCG GTCCAGAGAA CGCCACGTGT -ACTTTCCGT GGAGTTAGGC AACGGACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGTTGT GGCTCGGTAC
   ***** * * * * * * * * * * * * * * * * * * * * *
126 : GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG ACTCGTCTCT GGCTCGGCAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGGCCAAAG CTATATATGG
   ** *   ** * * * * * * * * * * * * * * * * * * * *
186 : GTTTAATACC TCGGTCGAGG CCGCCATGGC TTACGATGAA GCCGTAAGA AACTCTATGG

360 : TCAGTCTGCC AGACTCAATC TTCCCGAGAT CACAAATCGC TCTTCTTCCA CTGCTGCCAC
   ** ** * * * * * * * * * * * * * * * * * * * *
246 : ACACGAGGCT AAACCTCAA-C TTGGTGCACC CACAACAACA ACAACAAGTA GTAGTG-AAC

420 : TGCCACTGTG TCAGGCTC-G GTTACTGCAT TTTCTGATGA ATCTGAAGTT TGTGCACGTG
   * * * * * * * * * * * * * * * * * * * * * *
304 : AGAAACT-TG TCTTTTCTG GCCACGG--- -GTCGGGT-- -TCTGGGCT TAT-AATAAG

479 : AGGATACAAA TGCAAGTTCA GGTTTTGGTC AGGTGAAAC- TAGAGGATTG TAGCGATGAA
   * * * * * * * * * * * * * * * * * * * * * *
355 : AAGCTCGATA TG---GTTCA TGGGTTGGAC CTTGGTCTCG GCCAGGCAAG T--TGTTTAC

538 : TATGTTCT-- CTTAGATAGT TCTCAGTGTA TTA----AAG AGGA-GCTGA AAGGAAAAGA
   * * * * * * * * * * * * * * * * * * * * * *
410 : GAGGTTCTTG CTCAGAGAGA TC-GAGTTTT CTACAAGAAG ATGATGATCA TAGTCATAAT

591 : GGAAGTGAG- --GGAAGAAC ATAACCTGGC TGTGTTGTTT GGAATTGGAC A---GGAAGT
   ** ** *   ***   *   *   * * * * * * * * * *
469 : CGATGTTCTG CTTCAAGTGG TTCAATCTT TGTGTTGTTAT -TACCTAAAC AAAGTGATTC

645 : GAAAAG---G GAGACTTTGG ATGCT----- TGGTTGATG- -GGAATGGC AATGAACAAG
   **          ***** *   ***** * * * * * * * * * *
528 : ACAAGATCAA GAGACCGTTA ATGCTACGAC TAGTT-ATGG CGGTGAAGGC GGTGGTGGCT

695 : AACCATTGGA GTTT--GGTG TGGATGAAAC GTTTCATATT AATGAG---- --CTATTGGG
   * **   **** *   *****   ** **   *****   *** *
587 : CTACGTTAAC GTTTCGACC AATTTGAAAC CAAAGAATTT GATGAGTCAG AATTATGGAT

747 : TAT---ATTA AACGACAACA ATGTGTCT-- --GGTCAAG- --AGACAATG CAGTATCAAG
   *** ** * *   * * * * *   ** *****   *** * * * * *
647 : TATACAATGG AGTTTGGTCT AGGTTTCTTG TGGGGCAAGA AAAGAAGACG GAACATGACG

797 : TG-GATAGAC ACCCAAAT-T TCAGTTACCA AACGCAGTTT CCAAATTCTA ACTTGCTCGG

```

Fig. 4-26

0010181

```

707 :  ** ** * *      **  ** * * ** *      *** *      *** * **** *
      TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

855 :  GAGCCTCAAC CCTATGGAGA TTGCTCAACC AGGAGTT-GA TTATGGATGT CCTTATGTGC
      ***          ***      *** * *      ***** ** * **      *** **

767 :  GAG----- ----AGAGG ATGCATAGGC CGGAGTTGGA AGAGCGAACA GGATATTGCG

914 :  AGCCCACTGA ---TATGGAG AACTATGGTA TTGATTTAGA CCATCGCAGG TTCAATGATC
      *          ***      * ***** *      *** * * * *** *      ** *      *** **

815 :  AAATGGATGA TCTTTTGGAG ATTGATGATT TAGGTTT-GT TGATTG---- -GCAAAAATG

971 :  TTGACATACA GGAATTGGAT TTTGGAGGAG ACAAAGATGT TCATGGA--T CTACATAA
      ** * ** ** ***** ** ** ***      * * *      ***** *      * *

869 :  GAGA-TTTCA AGAATTGGTG TTGTGAAGAG TTTCA-ACAT CCATGGAATT GTTCTGTA

```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 48.34 [%]
Weight           : 62

```

```

1 :  ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
      *****
1 :  ATGCC----- CAGGAAACGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG

61 :  ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
      *****
46 :  ATTCTAAGGA AATGGAGAGA GTACAATGAG CAGACCGAGG CAGATTCTTG CATCGATGGT

121 :  GGTGGTCCAA AATCAATCCG AAAGCCTCCT CAAAAGGTT CGAGGAAGGG TTGTATGAAA
      *****
106 :  GGTGGTCCAA AACCAATCCG AAAGGCTCCT CAAAACGTT CGAGGAAGGG TTGTATGAAA

181 :  GGTAAGGTG GACCTGAAAA CGGGATTTGT GACTATAGAG GAGTTAGACA GAGGAGATGG
      *****
166 :  GGTAAGGTG GACCTGAAAA TGGGATTTGT GACTATACAG GAGTTAGACA GAGGACATGG

241 :  GGTAATGGG TTGCTGAGAT CCGTGAGCCA GACGGAGGTG CTAGGTTGTG GCTCGGTACT
      *****
226 :  GGTAATGGG TTGCTGAGAT CCGTGAGCCA GGCCGAGGTG CTAAGTTATG GCTCGGTACT

301 :  TTCTCCAGTT CATATGAAGC TGCATTGGCT TATGACGAGG CGGCCAAAGC TATATATGGT
      *****
286 :  TTCTCTAGTT CATATGAAGC TGCATTGGCT TATGATGAGG CTTCCAAAGC TATTTACGGT

361 :  CAGTCTGCCA GACTCAATCT TCCCGAGATC ACAAATCGCT CTTCTTCGAC TGCTGCCACT
      *****
346 :  CAGTCTGCCC GACTCAATCT TCC----- ----AC TG-----CT

```



Fig. 4-27

0010181

```

421 : GCCACTGTGT CAGGCTCGGT TACTGCATTT TCTGATGAAT CTGAAGTTTG TGCACGTGAG
*****
375 : GCCACTGTGT CAGGCTCGGT TACTGCATTT TCTGATGAAT CTGAAGTTTG TGCACGTGAG

481 : GATACAAATG CAAGTTCAGG TTTTGGTCAG GTGAACTAG AGGATTGTAG CGATGAATAT
*****
435 : GATACAAATG CAAGATCTGG TTTTGGTC-- -----

541 : GTTCTCTTAG ATAGTTCTCA GTGTATTAAA GAGGAGCTGA AAGGAAAAGA GGAAGTGAGG
** ****
463 : ----- --AGATCTC- -----

601 : GAAGAACATA ACTTGGCTGT TGGTTTTGGA ATTGGACAGG ACTCGAAAAG GGAGACTTTG
** ***
470 : -----TA ACT-----

661 : GATGCTTGGT TGATGGGAAA TGGCAATGAA CAAGAACCAT TGGAGTTTGG TGTGGATGAA
475 : -----

721 : ACGTTTGATA TTAATGAGCT ATTGGGTATA TTAACGACA ACAATGTGTC TGGTCAAGAG
** *
475 : -----TC T-----

781 : ACAATGCAGT ATCAAGTGGA TAGACACCCA AATTTTCAGTT ACCAAACGCA GTTTCCAAAT
****
478 : -----CGCA -TTTCCAA-

841 : TCTAACTTGC TCGGGAGCCT CAACCCATG GAGATTGCTC AACCAGGAGT TGATTATGGA
490 : -----

901 : TGTCTTTATG TGCAGCCCAG TGATATGGAG AACTATGGTA TTGATTAGA CCATCGCAGG
*** * ** *** * **** * * *** **
490 : -----ATG TTAAGTCCA- -----AT AACT---GCA TTGGTTAAG-

961 : TTCAATGATC TTGACATACA GGACTTGGAT TTTGGAGGAG ACAAAGATGT TCATGGATCT
**** ** *
520 : -----TTGG-----GGCGTT

1021 : ACATAA
** **
530 : AC-TAG

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

```

Fig. 4-28

0010181

Matching : 49.93 [%]  
Weight : 81

```

1 : ATG-----TC ATC--CATAG AG-----CCAAA
   ***          *** * * * *
1 : ATGGAAGAGG AAGATAACGG ATCGAAACAG AGTCCTCTG CTCTGTTGT ATCCTCGAGA

21 : AG-----TAA TGATGGTTG- ----GT---- ----GCTA- ----AT---- --AAGAA---
   **      **      *****      **      * * *      * *      *****
61 : AGACGAAGAA GAGTGGTTGA GCCAGTGGAA GCGACGTTAC AGAGATGGGA GGAAGAAGGA

48 : -----AC AACGAACCGT CCAAGCTA-- -GTTGAGGA AAGGTTGTAT GAGAGGAAAA
   *      * * * * *      *      *      *      *      *      *      *
121 : TTGGCGAGAG CTCGTAGGT TCAAGCCAAA GTTTCGAAGA AAGGTTGTAT GAGAGGAAAA

97 : GGTGGACCCG ATAACGCGTC TTGCACTTAC AAAGGTGTTA GACAACGCAC TTGGGGCAAA
   ***** * * * * *      *      *      *      *      *      *      *
181 : GGTGGACCAG AGAATCCTGT TTGTCGGTTT AGAGGTGTTT GACAAAGGT TTGGGGGAAA

157 : TGGGTCGCTG AGATCCGCGA GCC-----T AACCGAGGAG C-----TCGT-----
   ***** * * * * *      *      *      *      *      *      *      *
241 : TGGGTTGCTG AGATACGTGA ACCAGTGAGT CACCGTGGTG CAAACTCTAG TCCTAGTAA

196 : ---CTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CCTTGGCTTA TGACTCCGCA
   ***** * * * * *      *      *      *      *      *      *      *
301 : CGGCTTTGGC TTGGCAGCTT TGCTACTGCA GCTGAAGCTG CTTTGGCTTA CGACAGAGCT

253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTCCTT AAGAAGTTAC
   *** **      * * * * *      *      *      *      *      *      *      *
361 : GCTAGTGTCA TGTACGGACC CTATGCCAGG TTAAATTTC CGGAAGATT GGTGGGGGA

313 : CCTAAACCGG CGTCGTCTCC GCGTCCAG ACTACACCAA GCAGCAACAC CGGTGGAAAA
   * * * *      * * *      * * *      * * *      *      *      *      *
421 : AGGAAGAAG- -GACG----A GGAGCGGAA AGTTCGGGAG GC-----TAT TGGTTG-GAA

373 : AGCAGCAGCG ACTCTGAGTC GCCGTG-TTC ATCC--AAGC -AGATGTCAT CATGTGG--A
   * * * *      * * *      * * * *      * * * *      * *      *      *
469 : ACTAACAAG CCGGTAA--T GCGGTGATTG AAACGGAAGG TGGAAAAGAC TATGTAGTCT

427 : AGAGTGACAG AGGAGAT--A TCATGGGAGC AT-ATAA-AC GTGGA----T TTG-CCGGTA
   * * * *      * * *      * * * *      * * * *      * *      *      *
527 : ACAATGA-AG ACGCTATTGA GCTTGG--CC ATGACAAGAC TCAGAATCCT ATGACTGATA

478 : ATGGA----T G-ATTCTTCA ---ATATGGG AAGAA-GCTA CAATGTCGTT AGGATTTCCT
   *** *      * * *      * * *      * * * *      * *      *      *
584 : ATGAAATAGT GAACCCAGCA GTGAAATCAG AGGAAGGTTA CAGCTATGAT -CGATTCAAA

529 : TGGGTTTCATG AA--GGAG-A TAATGATATT TCTCGGTTTG ATACTTGTAT TTCCGGTGG-
   * * * *      * * *      * * * *      * *      *      *      *      *
643 : TTGGATAACG GATTGTTGTA TAATGA-ACC TCAAAGCT-- CCAGTTATCA CCAGGGAGGT

585 : CTATTCTAAT TGGGATTCCT TTCATTCCCC ACTTTGA
   **** * * *      * * *      * * *
700 : GGATTC-GAT TCATATTTTG AGTATTTTCA ATTCTAG

```

+++++

Sequence 1 : DREB2D.nuc  
Size : 621  
Matching Position : 1 - 621

Fig. 4-29

0010181

Sequence 2 : DREB2F.nuc  
 Size : 834  
 Matching Position : 1 - 834

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 46.13 [%]  
 Weight : 164

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***          *** ** *          * * ** * * * * * * *
1 : ATG----- --GAG--AA A----- --TCATCCTC A-ATGAAACA A-----

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
   * ** * * * * * * * * * * * * * * * * * * * * * *
28 : -----T GGAAGAAGGG TCCTGCTCGG GGTAAGGCG GTCCACAAAA CGCTCTTTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
   *** * * * * * * * * * * * * * * * * * * * * * *
79 : CAGTACCGTG GAGTCAGGCA AAGGACTTGG GGCAAATGGG TGGCTGAGAT CAGAGAGCCC

181 : AA-CCGAGGA GCTCGTCTTT GGCTCGGTAC CTTGCACACC TCCCGTGAAG CTGCCTTGGC
   ** **** ** * **** **** ** * **** ** * **** * * *
139 : AAGAAGAGG- GCAAGACTTT GGCTTGGCTC TTTCGCTACA GCTGAAGAAG CAGCTATGGC

240 : TTATGACTCC GCAGCTCGTA AGCTCTATGG GCCTGAGG-- ----- --CTCATCT
   ***** ** ** * * ***** ** ** * *****
198 : TTATGATGAG GCTGCCTTGA AACTCTATGG GCACGACGCA TACCTCAACT TACCTCATCT

285 : ----- -CAA---CCT CCCTGAGT-- CCTTAAGAAG T----- TACCCTAAA-
   *** * * * * * * * * * * * * * * * * * * * *
258 : TCAGCGGAAT ACAAGACCTT CTCTGAGTAA CTCTCAGAGG TTCAAATGGG TACCTTCAAG

319 : -----ACG GCGTCGTCTC C-----GG -----C GT-----CCC AGACT-----
   * * * * * * * * * * * * * * * * * * * * *
318 : GAAGTTTATA TCTATGTTTC CTTCATGTGG TATGCTAAAC GTGAATGCTC AGCCTAGTGT

346 : --ACACCAAG CAGC-AACAC CGGTGGAA-- ----AAAGC- -----
   *** * **** * * * * * * * * * * * * * * *
378 : TCACATAATC CAGCAAAGAC TAGAAGAACT CAAGAAAACCT GGACTTTTAT CTCAATCCTA

376 : -----AG- -----CA GCG----- -ACTCTGAGT CGCCGTGTTT AT-----C
   **          ** **          *** * * ** * * * *
438 : TTCTTCTAGT TCTTCCTCCA CCGAATCAAA AACTAATACT AGCTTTCTTG ATGAGAAGAC

405 : CAAC----GA GA---TGTCA TCATG-TGGA AG--AGTGA- CAGAGG---- -AGATAT---
   ** * ** ** * ** *** * * * * **** * * * *
498 : CAGCAAGGGA GAAACAGACA ATATGTTTCA AGGTGGTGAT CAGAAGAAAC CAGAGATCGA

446 : CATG----- --GGAGC A--TA----- --TAAACG-T GGATTTG--- ----CC---
   * **          *** * *          * * * * * * *
558 : CCTGACCGAG TTTCTTCAGC AACTAGGAAT CTTGAAGGAT GAAAATGAAG CAGAACCAAG

474 : ---GGTAATG GA---TGATT ---CTTCAAT ATGG----- ---GAAGAAG CTACAATGTC
   **** ** * *** ** ** ****          ***** ** **
618 : TGAGGTAGCA GAGTGTCAAT CCCCTCCACC ATGGAACGAG CAAGAAGAAA CTGGAA-GTC
  
```

Fig. 4-30

0010181

```

516 : GTT----- --AGGATTTC -CATGGGTT- -CATGAAGGA GAT----- AATGA-----
      **          ** *****      * * * * * ** * * * * *
677 : CTTTCAGAAC TGAGAATTTC AGCTGGGATA CCCTGATCGA GATGCCAAGA AGTGAAACCA

552 : -TATTTCTCG GTTTGATACT TGTATTTCCG GTGGCTATTC TAATTGGGAT -----TCCT
      * * * * * ***** * * * * * * * * * * * * * * * * * * * * * *
737 : CAACTATGCA ATTTGACTCC AGCAACTTCG GAAGCTATGA TTTGAGGAT GATGTATCCT

605 : TTCATTCC-- -----CCAC T----- --TTGA
      * * * * * * * * * * * * * * * *
797 : TCCCTTCCAT CTGGGACTAC TACGGAAGCT TAGATTGA

```

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```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 45.04 [%]
Weight       : 190

```

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***          ** ** ** * * * * * * * * * * * * * * * * *
1 : ATG----- --GA-AGAAG AGCAA----- ---CCTCCGG CCAAGA---A ACGAAACAT-

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
     * ** * * * * * * * * * * * * * * * * * * * * * * * * * *
39 : --GGGGAGAT CTAGAAAAGG TTGCATGAAA GGTAAAGGCG GTCCAGAGAA CGCCACGTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
     **** * * * * * * * * * * * * * * * * * * * * * * * * * *
97 : ACTTCCGTG GAGTTAGGCA ACGGACTTGG GGTAAATGGG TGGCTGAGAT CCGTGAGCCT

181 : AACCAGGAG CTGCTCTTTG GCTCGGTACC TTCGACACCT CCCGTGAAGC TGCCTTGGCT
     ***** ** ***** ** ***** ** * * * * * * * * * * *
157 : AACCCTGGGA CTGCTCTCTG GCTCGGCACG TTTAATACCT CGGTGAGGC CGCCATGGCT

241 : TATGACTCCG CAGCTCGTAA GCTCTATGGG CCTGAGGCTC ATCTCAAC-- ----CTCCCT
     ** ** * * * * * * * * * * * * * * * * * * * * * * *
217 : TACGATGAAG CCGCTAAGAA ACTCTATGGA CACGAGGCTA AACTCAACTT GGTGCACCCA

295 : GA-----GTC CTTAAGAAGT --TACCCTAA AAC----- --GGC-- --GTCG--
     * * * * * * * * * * * * * * * * * * * * *
277 : CAACAACAAC AACAAGTAGT AGTGAACAGA AACTTGTCTT TTTCTGGCCA CGGGTCGGGT

328 : TCTCCGGC-- -----G TC---CCAG
     *** ** * * * * * * * * * * * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG

343 : AC-----TA CACCAAG--- -----CAGCA ACACCG---G TGGAAAAAGC AGCAGCGACT

```

Fig. 4-31

```

                                0010181
      *   *   *   *   *   *   *   *   *   *   *   *   *
397 : GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT

386 : CTGAGTC--- -GCCGTGTTC ATC--CAA-- ----CGA--- ---GAT-GTC ATCATGTGGA
      *   ****   *   ***** **   ***   ***   *   *   *   *   *
457 : CATAGTCATA ATCGATGTTC GTCTTCAAGT GGTTCGAATC TTTGTTGGTT ATTACCTAAA

427 : -AGAGTGA-- CAGAGGA--- -----GA -TA-TCATGG ----GA----
      *   ***** **   *   *   *   *   *   *   *   *   *   *
517 : CAAAGTGATT CACAAGATCA AGAGACCGTT AATGCTACGA CTAGTTATGG CGGTGAAGGC

453 : -----GC- --ATATAAAC GT----- -----GGATTT GCCG-GT---
      **   *   *   *   *   *   *   *   *   *   *   *   *
577 : GGTGGTGGCT CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG

477 : -----AATGG -----ATGATTCTT- ----CAATA TGGGAAGAAG
      *   *   *   *   *   *   *   *   *   *   *   *   *
637 : AATTATGGAT TATACATGG AGCTTGGTCT AGGTTTCTTG TGGGCAAGA AAAGAAGACG

506 : CTACA----- --AT-GTC GTTAGGAT-- -----TTCC-
      ***   **   *   *   *   *   *   *   *   *   *   *
697 : GAACATGACG TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCCT

528 : -----ATGGGT TCAT----- --GAAG ---GA----G ATA-----
      **   *   *   *   *   *   *   *   *   *   *   *   *
757 : AGTTGCCGCG GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTTGGAA

548 : ---ATGATA TTTCTCGGTT TGAT-ACTT- -GTATTTCCG GTGGCTA--- -----TTC
      ***** ***   *   *   *   *   *   *   *   *   *   *
817 : ATGGATGATC TTTTGGAGAT TGATGATTTA GGTGTTGTTA TTGGCAAAA TGGAGATTC

591 : --TAATTGG- ----GATTC CTTTCATTCC CCA----- --CTTTGA
      ***** **   ***** ***   *   *   *   *   *
877 : AAGAATTGGT GTGTGAAGA GTTCAACAT CCATGGAATT GGTTCGTA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps             : 1
*N+              : 2

Matching         : 47.49 [%]
Weight          : 113

```

```

1 : ATG----- TCAT----- CCA---TAG -----AGCCA----
    ***          ** *   * *   ***   ** *
1 : ATGCCCAAGG AACGGAAGTC TCGTGAACA CGAGATGTAG CTGAGATTCT AAGGAAATGG

19 : --AAAGT--A ATG----- --ATGG TTGGTGCT-A ATAAGAAACA
     *   *   *   *   *   *   *   *   *   *   *   *
61 : AGAGAGTACA ATGAGCAGAC CGAGGCAGAT TCTTGATCG ATGGTGGTGG TTCAAACCA

```

Fig. 4-31

0010181

```

*      *   * * *   *      * * *   *   *   *   *   *
397 : GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT

386 : CTGAGTC--- -GCCGTGTTT ATC--CAA-- ----CGA--- ---GAT-GTC ATCATGTGGA
*   ****   *   ***** **   ***   ***   *   *   *   *   *
457 : CATAGTCATA ATCGATGTTT GTCTTCAAGT GGTTCGAATC TTTGTTGGTT ATTACCTAAA

427 : -AGAGTGA-- CAGAGGA--- -----GA -TA-TCATGG ----GA----
*   ***** **   *   *   *   *   *   *   *   *   *   *
517 : CAAAGTGATT CACAAGATCA AGAGACCGTT AATGCTACGA CTAGTTATGG CGGTGAAGGC

453 : -----GC- --ATATAAAC GT----- -----GGATTT GCCG-GT---
**   *   *   *   *   *   *   *   *   *   *   *   *
577 : GGTGGTGGCT CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG

477 : -----AATGG -----ATGATTCTT- ----CAATA TGGGAAGAAG
***** **   *   *   *   *   *   *   *   *   *   *
637 : AATTATGGAT TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGCAAGA AAAGAAGACG

506 : CTACA----- -AT-GTC GTTAGGAT-- -----TTCC-
***   **   *   *   *   *   *   *   *   *   *   *
697 : GAACATGACG TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCTT

528 : -----ATGGGT TCAT-----GAAG ---GA---G ATA-----
**   *   *   *   *   *   *   *   *   *   *   *
757 : AGTTGCCGCG GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTTGGAA

548 : ---ATGATA TTTCTCGGTT TGAT-ACTT- -GTATTTCCG GTGGCTA--- -----TTC
***** ***   *   *   *   *   *   *   *   *   *   *
817 : ATGGATGATC TTTTGAGAT TGATGATTTA GGTGTTGTTA TTGGCAAAAA TGGAGATTTT

591 : --TAATTGG- ----GATTC CTTTCATTCC CCA----- --CTTTGA
***** **   *   *   *   *   *   *   *   *   *   *
877 : AAGAATTGGT GTTGTGAAGA GTTTCAACAT CCATGGAATT GGTTCGTA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 47.49 [%]
Weight            : 113

```

```

1 : ATG----- TCAT----- CCA----TAG -----AGCCA----
***   **   *   *   *   *   *   *   *   *
1 : ATGCCCGAGGA AACGGAAGTC TCGTGGAACA CGAGATGTAG CTGAGATTCT AAGGAAATGG

19 : --AAAGT--A ATG-----ATGG TTGGTGCT-A ATAAGAAACA
*   ***   *   *   *   *   *   *   *   *
61 : AGAGAGTACA ATGAGCAGAC CGAGGCAGAT TCTTGCATCG ATGGTGGTGG TTCAAACCA

```

```

207 : GTTTAGA--- -GGTGT--- -CGACAAAGG GT-----T TGGG--GGAA ATGGGTTGCT
    *   ***   ** **   * * * * *   *   ****   *   *   *   ***
300 : GAACAGAAAC TTGTCTTTTT CTGGCCACGG GTCGGGTTCT TGGGCTTATA ATAAGAAGCT

250 : GAGATACGTG AACCAGTGAG TCACCGTGGT ---GCAAACT CTAGTCGTAG TAAACGGCTT
    **** * *   * * *   *** ****   *   *   *   *** **   *   * *
360 : -CGATATG-G TTCATGGGT GGACCTTGGT CTCGGCCAGG CAAGTTGT-T CACGAGGTTT

307 : TGGCTTGG-- ----CACGTT TGCTAC-TGC AGCTGAAGCT GCTTTGGCTT ACGACAGAGC
    *   *** *   *   *** * **** *   ** *** * *   *   *   *   *   *
417 : TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT -CATAGTCAT A----ATCGA

360 : TGCTAGT-GT CA--TGTACG GACCCTATGC CAGGTAAAT TTCCCGGAAG ATTTGGGTGG
    ** * * * * *   ** ** **   **** ** * * *   *   *   *   *
472 : TGTTCTGCTT CAAGTGGTTC GAATCTTTG- TTGGTT--AT TACCTAAACA AAGTGATTCA

417 : GGGAAGGAAG AAGGACG--- AGGAGGCGGA AAGTTCGGGA GGCTATTG-G TTGAAACT-
    *   *** ** **   * *   **   **** ** ** * * *   *** **
529 : CAAGATCAAG -AGACCGTTA ATGCTACGAC TAGTTATGGC GGTGAAGGCG GTGGTGGCTC

472 : AACAAAGCCG GTAATGGCGT GATTGAAACG GAAG--GTGG AAAAG----- ACTATGTAGT
    **   ** * * *   *   *   *   **** * * *   *   *   *   *   *
588 : TACGTTAACG TTTTCGACCA ATTTGAAACC AAAGAATTGG ATGAGTCAGA ATTATGGATT

```

60/94

Fig. 4-34

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0010181

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 45.74 [%]
Weight       : 200

```

```

1 : ATGGAAGG A-----A GATAACGGAT CGAAACA--- -GAGCTC--- ----CTCTGC
    ***** * * *   *   *   *   *****   *** **   ***
1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGTTGC

42 : TTCTGTTGTA -----TCC TCGAGAAGAC GAAGAAGA-- ----GTGG-T TGAGCCAGTG
    *   ***   ***   ***** *   *   *   ****   *   *   *   *
61 : ATGAAAGGTA AAGGCGGTCC -AGAGAACGC CACGTGTACT TTCCGTGGAG TTAGGCAACG

88 : GAAGCGACGT TA----- CAGAGAT--G GGAG--GAA- -GAAGGA-TT GGCGAGAGCT
    ** * * *   *   ***** *   *** **   *   *** *   *   ***
120 : GACTTGGGGT AAATGGGTGG CTGAGATCCG TGAGCCTAAC CGTGGGACTC GTCTCTGGCT

133 : CGTAGGGTTC AA----- ----GC CAAAGGTT-C GAAGAA----- -AGGTT
    **   *** **   *   *   *   *   *   *   *   *   *   *   *
180 : CGGCACGTTT AATACCTCGG TCGAGGCCGC CATGGCTTAC GATGAAGCCG CTAAGAAACT

```

```

525 : CTACAATGAA G---ACGCTA ---TTGAGCT TGGCCATGAC AAGA-----
      ***** * .   ***   *   *   *   *   *   *   *   *   *
648 : ATACAATGGA GCTTGGTCTA GGTTTCTTGT GGGGCAAGAA AAGAAGACGG AACATGACGT

563 : CTCA----- ---GAATCCT ATGACTGATA ATGA-AATA- GT--GAACCC AG-----
      ***           *   *   *   *   *   *   *   *   *   *   *   *
708 : GTCATCGTCG TGTGGATCGT CGGAC-AACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

602 : --CAGTGAAA TCAGAGGAAG --GTT---AC AGC---TATG ATCGATTCAA A-----
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
767 : GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTGGAA ATGGATGATC

643 : --TTGGATAA CG--GATTGT TGTATAATGA ACCTCAAAGC TCCAGTTATC ACCA--GGGA
      ***** *   *****   *   *   *   *   *   *   *   *   *
827 : TTTTGGAGAT TGATGATTGA GGTGTGTTGA TTGGCAAAAA TGGAGATTTC AAGAATTGGT

697 : GGTG-GATTC GATTCATATT TTGAGTATTT CAGATTCTAG
      *   *   *   *   *   *   *   *   *   *   *   *   *
887 : GTTGGAAGA GTTCAACAT CCATGGAATT --GGTCTGA

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatched       : 1
Gaps             : 1
*N+              : 2

Matching         : 48.72 [%]
Weight          : 93

```

```

1 : AT-----GGA AAAGGAAGAT AACGGATCGA A-AC-AGA-G CTCCTCTGCT TCTGTTGTAT
   **   *** ** *   *   *   *   *   *   *   *   *   *   *   *
1 : ATGCCCAGGA AACGGAAG-T CTCG--TGGA ACACGAGATG TAGCTGAGAT TCTAAGGAA-

53 : CCTCGAGAAG ACGAAGAAGA GTGGTTGAGC CAGTGAAGC GACGTTACAG AGATGGGAGG
   *   *   *   *   *   *   *   *   *   *   *   *   *   *
57 : -ATGGAG-AG AGTACAATGA G-----CAGA CCGAGGCAGA TTC-TTGCAT CGATGG----

113 : AAGAAGGATT GGCGAGAGCT CGTAGGGTTC AAGCCAAAGG TTCGAAGAAA GGTTGTATGA
     *   *   *   *   *   *   *   *   *   *   *   *   *
105 : -TGTTGGTTC AAAACCAATC CGAAAGGCTC CTCCAAACG TTCGAGGAAG GGTTGTATGA

173 : GAGGAAAAGG TGGACCAGAG AATCCTGTTT GTCGGTTTAG AGGTGTTCCA CAAAGGGTTT
     *** ***** ** *   *   *   *   *   *   *   *   *   *
164 : AAGGTAAAGG TGGACCTGAA AATGGGATTT GTGACTATAC AGGAGTTAGA CAGAGGACAT

233 : GGGGGAATG GGTGCTGAG ATACGTGAAC CAGTGAGTCA CCGTGGTGCA AACTCTAGTC
     **** ***** ** *   *   *   *   *   *   *   *   *
224 : GGGGTAAATG GGTGCTGAG ATCGTGAGC CAG-----G CCGAGGTGC- -----

293 : GTAGTAAACG GCTTTGGCTT GGCACGTTTG CTAAGCTGCT TGAAGCTGCT TTGGCTTACG

```



Fig. 4-35

0010181

```

525 : CTACAATGAA G---ACGCTA ---TTGAGCT TGGCCATGAC AAGA-----
      ***** * *      ***      ** * ** * ** *
648 : ATACAATGGA GCTTGGTCTA GGTTTCTTGT GGGGCAAGAA AAGAAGACGG AACATGACGT

563 : CTCA----- ---GAATCCT ATGACTGATA ATGA-AATA- GT--GAACCC AG-----
      ***      * *** *      *** * * * * * ** * * *
708 : GTCATCGTCG TGTGGATCGT CGGAC-AACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

602 : --CAGTGAAA TCAGAGGAAG --GTT---AC AGC---TATG ATCGATTCAA A-----
      * * * * * ** * * * * * *** * * * * * * * * *
767 : GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTGGAA ATGGATGATC

643 : --TTGGATAA CG--GATTGT TGTATAATGA ACCTCAAAGC TCCAGTTATC ACCA--GGGA
      ***** * * **** * * * **** * * * * * * * *
827 : TTTTGGAGAT TGATGATTTA GGTTTGTGTA TTGGCAAAAA TGGAGATTTC AAGAATTGGT

697 : GGTG-GATTG GATTGATATT TTGAGTATTT CAGATTCTAG
      * * * * * * * * * * * * * * * * *
887 : GTTGGAAGA GTTCAACAT CCATGGAATT --GGTCTGA

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

## Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 48.72 [%]
Weight            : 93

```

```

1 : AT-----GGA AAAGGAAGAT AACGGATCGA A-AC-AGA-G CTCCTCTGCT TCTGTTGTAT
  **      *** ** ***** * ** * * * * * * * * * *
1 : ATGCCCAGGA AACGGAAG-T CTCG--TGGA ACACGAGATG TAGCTGAGAT TCTAAGGAA-

53 : CCTCGAGAAG ACGAAGAAGA GTGGTTGAGC CAGTGGAAGC GACGTTACAG AGATGGGAGG
    * * * * * * * * * * * * * * * * * * * *
57 : -ATGGAG-AG AGTACAATGA G-----CAGA CCGAGGCAGA TTC-TTGCAT CGATGG----

113 : AAGAAGGATT GGCGAGAGCT CGTAGGGTTC AAGCCAAAGG TTCGAAGAAA GGTGTATGA
     * * * * * * * * * * * * * * * * * * * *
105 : -TGGTGGTTC AAAACCAATC CGAAAGGCTC CTCCAAACG TTCGAGGAAG GGTGTATGA

173 : GAGGAAAAGG TGGACCAGAG AATCCTGTTT GTCGGTTTAG AGGTGTTTGA CAAAGGGTTT
     *** ***** ** * * * * * * * * * * * * *
164 : AAGGTAAAGG TGGACCTGAA AATGGGATTT GTGACTATAC AGGAGTTAGA CAGAGGACAT

233 : GGGGGAAATG GGTGCTGAG ATACGTGAAC CAGTGAGTCA CCGTGGTGCA AACTCTAGTC
     **** ***** ***** ** * * * * * * * * *
224 : GGGGTAAATG GGTGCTGAG ATCCGTGAGC CAG-----G CCGAGGTGC- -----

293 : GTAGTAAACG GCTTTGGCTT GGCACGTTTG CTACTGCAGC TGAAGCTGCT TTGGCTTACG

```

Fig. 4-36

0010181

```

267 : ----TAA--- GTTATGGCTC GGTACTTTCT CTAGTTCATA TGAAGCTGCA TTGGCTTATG
          *** * * ***** ** * * * *** * * * ***** *
353 : ACAGAGCTGC TAGTGTCTAG TACGGACCCT ATGCCAGGTT AAATTTCCCG GAAGATTGCG
          * *** * * * * ***** * * ***** * * *** * *
320 : ATGAGGCTTC CAAAGCTATT TACGGTCAGT CTGCCCGACT CAATCTTCC- -----
          * * * * *
413 : GTGGGGGAAG GAAGAAGGAC GAGGAGGCGG AAAGTTCGGG AGGCTATTGG TTGGAAACTA
          * * * * *
369 : -----AC -----TGCTG CCACTGTGTC AGGC--TCGG TT----ACT-
          * * * * *
473 : ACAAAGCCGG TAATGGCGTG ATTGAAACGG AAGGTGGAAA AGACTATGTA GTCTACAATG
          * * * * *
399 : -----GC--- --ATTTTCTG A-TGAATCTG AAG----- --TTTGT- -----
          * * * * *
533 : AAGACGCTAT TGAGCTTGGC CATGACAAGA CTCAGAATCC TATGACTGAT AATGAAATAG
          * * * * *
426 : -----GCACG TGAG----- -----GAT A--CAAAT--
          * * * * *
593 : TGAACCCAGC AGTGAAATCA GAGGAAGGTT ACAGCTATGA TCGATTCAAA TTGGATAACG
          * * * * *
444 : -----GC A--AGATC- -----TGGTT -TTGGTCAGA TC---TCTAA CT---TCTCG
          * * * * *
653 : GATTGTTGTA TAATGAACCT CAAAGCTCCA GTTATCACCA GGGAGGTGGA TTCGATTGAT
          * * * * *
480 : CAT--TTCCA AAATG---T TAA--GTCCA ---ATAAC-- -----TGCA TTGG-----
          * * * * *
713 : ATTTTGAGTA TTTCAGATTC TAG
          * * * * *
515 : ---TTAAGTT GGGGCGTTAC TAG
          * * * * *

```

+++++

```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
* N +            : 2

Matching          : 54.15 [%]
Weight           : 19

```

```

1 : ATGG-AGAA- ATCATCCTC- -----AA TGAACAATG GAAG----- -AAGGGTCTT
    **** * * * * *
1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGT--T
    **** * * * * *

43 : GCTCG--GGG TAAAGGCGGT CCACAAAACG CTCTTTGTCA GTACCGTGGA GTCAGGCAAA
    * * * * *
59 : GCATGAAAGG TAAAGGCGGT CCAGAGAACG CCACGTGTAC TTTCCGTGGA GTTAGGCAAC
    * * * * *

101 : GGAAGTGGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC
    *****

```

Fig. 4-37

0010181

```

119 : GGACTTGGGG TAAATGGGTG GCTGAGATCC GTGAGCCTAA CCGTGGGACT CGTCTCTGGC
161 : TTGGCTCTTT CGCTACAGCT GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC
    * * * * *
179 : TCGGCACGTT TAATACCTCG GTCGAGGCCG CCATGGCTTA CGATGAAGCC GCTAAGAAAC

221 : TCTATGGGCA CGACGCATAC CTCAACTT-- -----ACC TCATCTTCAG C-----
    ***** ** * * * * *
239 : TCTATGGACA CGAGGCTAAA CTCAACTTGG TGCACCCACA ACAACAACAA CAAGTAGTAG

263 : GGAATACAA- ---GACCTTC TCTGAGTAAC ---TC----T C-AGAGGTTC AAATGGGTAC
    * * * * *
299 : TGAACAGAAA CTTGTCTTTT TCTG-GCCAC GGGTCGGGT CTTGGGCTTA TAATAAGAAG

311 : CTTCAAGGAA GTTTAT---- ---ATCTATG TTTCCTTCAT G--TGGTATG CTAAACGTGA
    * * * * *
358 : C-TCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG GCAAGTTGTT CACGAGGTTC

362 : ATGCTCAGCC TAGTGTTCAC ATAATCCAGC AAAGACTAGA AGAACTCAAG AAAACTGGAC
    ***** ** * * * * *
417 : TTGCTCAG-- -AGAGATCGA GTTTTCTA-C AAGAAGATGA TGATCATAGT CATAATCGAT

422 : TTTTATC-TC AA----TCCT ATTCTT--CT AGTTCTT-CC TCCACCGAAT CAAAACTAA
    * * * * *
473 : GTTCGTCTTC AAGTGGTTCG AATCTTTGTT GGTATTACC TAAACAAAGT GATTCAACA

474 : TACTAGCTTT C-TTGATGAG AAGACCAGCA AGGGAGAAAC AGACAAT---- --ATGTTG-
    * * * * *
533 : ATCAAGAGAC CGTTAATGCT ACGACTAGTT ATGGCGGTGA AGGCGGTGTT GGCTCTACGT

527 : -AAGGTGGT- GATC-AGAAG AAACCAGAGA --TCGACCTG ACCGAGTTTC TTCAGCA-AC
    * * * * *
593 : TAACGTTTTT GACCAATTTG AAACCAAGA ATTTGATGAG TCAGA-ATTA TGGATTATAC

581 : TAGGAATCTT G--AAGGAT GAAATGAAG CAGAACCAAG TGAGGTAGCA -GA-GTGTCA
    * * * * *
652 : AATGGAGCTT GGTCTAGGTT TCTTGTGGG CAAGAAAAGA AGACGGAACA TGACGTGTCA

636 : T--TCCCCTC CACCATGGAA CGAGCAAGAA GAACTGGAA GTCCTTTCAG AACTGAGAAT
    * * * * *
712 : TCGTCGTGTG GATCGTCGGA C-AACAAGGA GA----GTAT GTTGGTTC-- --CT---AGT

694 : TTCAGCTGGG ATACCTGAT CGAGATGCCA AGAAGTAAA CCACAACAT GCAATTTG--
    * * * * *
760 : TCGGCGGAG AGA---GGAT GCATAGGCC- GGAGTTGGA GAGCGAACAG GATATTTGGA

752 : ACTCCAGCAA CTTGGAAGC T--ATGATT- -----TTG A--GG--ATG ATGTATCCTT
    * * * * *
816 : AATGGATGAT CTTTGGAGA TTGATGATT AGGTTTGTG ATTGGCAAAA ATGGAGATT

798 : C---CCTTCC ATCTGGG--- -----ACT ACTACGGAAG CTTAGAT-TG A
    * * * * *
876 : CAAGAAITGG TGTGTGAAG AGTTTCAACA TCCATGGAA- -TTGGTTCTG A
  
```

+++++

```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

Sequence 2      : DREB2H.nuc
  
```

Fig. 4-38

0010181

Size : 534  
 Matching Position : 1 - 534

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 41.63 [%]  
 Weight : 254

```

1 : ATGGAGAAAT CATCCTCAAT GAAACAATGG AAGAAGGGTC CTGCTCGGGG TAAAGGCGGT
   ***          * * ***** ** ***          **** ** **
1 : ATG----- ----CCCAG GAAAC---GG AAG----- --TCTCGTGG --AA-----

61 : CCACAAAACG CTCTTTGTCA GTACCGTGGA GTCAGGCCAA GGACTTGGGG CAAATGGGTG
   *** * *          ***          * * * * * * * * * *          *****
29 : -CACGAGA-- ----TGT-- ----AGCTGA G--ATTCTAA GG----- -AAATGG--

121 : GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC TTGGCTCTTT CGCTACAGCT
      * ***** ** * ***          **** *** * *****
61 : -----A GAGAGTACA- -ATGAG---C AGACCGAGGC -AGATTCTT- -----

181 : GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC TCTATGGGCA CGACGCATAC
      *** * ***** ** **          ** *** * * * * * * * * * *
95 : -----GCAT CGATGG---- TGGTG----- --GTTCAAAA CCAATCCGAA AGGCTCCT-C

241 : CTCAACTTAC CTCATCTTCA GCGGAATACA AGACCTTCTC TGAGTAACTC TCAGAGGTTT
      * ***          *** * *****          * ** * * * * * *
137 : CAAAAC--- ----GTTC- GAGGAA--- ----- -GGGT-TGTA TGAAGGT--

301 : AAATGGGTAC CTTCAAGGAA GTTTATATCT ATGTTTCCTT CATGTGGTAT GCTAA--ACG
      *** * * * * *          *** * * * * * * * * * * * * * * *
169 : AAAGGTGGAC CT-----GAA AATGGGATTT GTGACT-ATA CAGGAGTTAG ACAGAGGACA

359 : TGAATGCTCA GCCTAGTGTT CACATAATCC AGCAAAGACT AGAAGAACTC AAGAAAACCTG
      ** * * * *          ** * * * *          *** * * * * * * * *
223 : TG--GGGTAA ATGGGTGCTG GAGATCCGTG AGCCAGGCC- -GAGGTGCT- AAG-----

419 : GACTTTTATC TCAATCCTAT TCTTCTAGTT CTTCTCCAC CGAATCAAAA ACTAATACTA
      ** * * * * * * * * * *          * * * * * * * *
271 : ---TTATGGC TCGGTACT-T TC-TCTAGTT C----- --ATATGAA GCT-GCATTG

479 : GCTTTCTTGA TGAGAAGACC AGCAAGGGAG AAACAGACAA TATGTTGAA GGTGGTGATC
      **** *** ***** ** * *** *          ** * * * * * * * *
313 : GCTT--ATGA TGAGGCTTCC A--AAGCTAT TTACGGTCAG TCTGCCCGA- -----C

539 : AGAAGAAACC AGAGATCGAC CTGACCGAGT TTCTTCAGCA ACTAGGAATC TTGAAGGATG
      ** ** * * *          *** **          ** *          *** * * * *
359 : TCAATCTTCC ACTGCTGCCA CTGTGTCAG- --GCTCGGTT ACT--GCATT TT--CTGATG

599 : AAAATGAAGC AGAACCAAGT GAGGTAGCAG AGTGTGATTC CCCTCCACCA TGAACGAGC
      ** *****          ** ** *****          **          ** * **
412 : AATCTGAAGT TTGTGCACGT GAGG----- ----AT-- ----AC-- ----AAATGC

659 : AAGAAGAAAC TGGAAGTCCT TTCAGAACTG AGAATTTGAG CTGGGATACC CTGATCGAGA
      *** * * * *          * ** * * * * * * * *          ** ** ***
446 : AAG-----ATC TGG-----T TTTGG---TC AG-ATCTC-- -----TA-A CTTCTCGCAT

```

Fig. 4-39

```

                                -0010181
719 : TGCCAAGAAG TGAAACCACA ACTATGCAAT TTGACTCCAG CAACTTCGGA AGCTATGATT
    * ****                ***    * * ****    ****    **    ***
483 : TTCCAA----- --AATG--- TTAAGTCCAA TAACT----- -GC---ATT

779 : TTGAGGATGA TGTATCCTTC CCTTCCATCT GGGACTACTA CGGAAGCTTA GATTGA
    * * * **                * *** * * * *    ** *
513 : -----GGTTA AGT-----T GGGGC-GTTA C-----TA G-----

+++++

Sequence 1          : DREB2G.nuc
  Size              : 924
  Matching Position : 1 - 924

Sequence 2          : DREB2H.nuc
  Size              : 534
  Matching Position : 1 - 534

Matching Condition.

Matches           : -1
Mismatches        : 1
Gaps              : 1
*N+               : 2

Matching          : 38.38 [%]
Weight           : 325

1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGTTGC
  **                * *** **** * * * *    * * * *    * * * *
1 : AT----- GCCCAGGAAA CGGAAGTCTC GTGGAAC-AC GAGATGTAGC

61 : ATGAAAGGTA AAGGCGGTCC AGAGAACGCC ACGTGTACTT TCCGTGGAGT TAGGCAACGG
  *** *      **** *      ****          **** * * * *      ***** *
42 : -TGAGATTCT AAGGAAATGG AGAGA----- ----GTACAA TGAGCAGACC GAGGCA---G

121 : ACT-TGGGGT AAATGGGTGG CTGAGATCCG TGAGCCTAAC CGTGGGACTC GTCTCTGGCT
  * * * * *    ** ***** ** * *    * * * * *    * * * *    **
89 : ATTCTTGCAT CGAT-GGTGG -TG-GTTC-- AAAACCAATC CGAAAGGCTC -----CT

180 : CGGCACGTTT AATACCTCGG TCGAGGCCGC CATGGCTTAC GATGAAGCCG CTAAGAAACT
  * **      **      ****          * * * *    * * * *
136 : C--CA----- AA----ACGT TCGAGG---- -AAGGGTT-- -----GTATGAAA--

240 : CTATGGACAC GAGGCTAAAC TCAACTTGGT GCACCCACAA CAACAACAAC AAGTAGTAGT
  * ****          *** * ***
166 : -----GGTAAA- -----GGT GGACC-----T

300 : GAACAGAAAC TTGTCTTTTT CTGGCCACGG GTCGGGTTCT TGGGCTTATA ATAAGAAGCT
  **      ***          *** * * * * *    * * * *    * * * *
181 : GA---AAA- -----TGGGAT-T TGTGACTATA --CAGGAGTT

360 : CGATATGGTT CATGGGTTGG ACCTTGGTCT CGGCCAGGCA AGTTGTTTAC GAGGTTCTTG
  ** * *    ***** *    ***          **** *    *** * * *
211 : AGACAGAGGA CATGGGGTAA A---TGG--- -GTTGCT--- GAGATCCGTG

420 : CTCAGAGAGA TCGAGTTTTT TACAAGAAGA TGATGATCAT AGTCATAATC GATGTTCTGC
  ** **      ****          ** ***      ***
251 : ---AGCCAGG CCGAG----- -GTGCTAA-- ---GTT-----

480 : TTCAAGTGGT TCGAATCTTT GTTGGTTATT ACCTAAACAA AGTGATTAC AAGATCAAGA

```

Fig. 4-40

0010181

```

273 :   ***   ***   ****   *           ***
      -----ATGGC TCGGTACTTT CT----- --CTA-----

540 :   GACCGTTAAT GCTACGACTA GTTATGGCGG TGAAGGCGGT GGTGGCTCTA CGTTAACGTT
      *** *           ****           * * *   ***** ** * * * *
293 :   ----GTTCA- ----- --TATG---- ---AAGCTGC ATTGGCT-TA TGATGAGGCT

600 :   TTCGACCAAT TTGAAACCAA AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC
      *           **** **   ** * *   *****   ** *   **** *
328 :   T----- --CCAA AGCTATTTAC G-GTCAG--- TCTGCCCGAC TCAAT---C

660 :   TTGGTCTAGG TTTCTTGTGG GGCAAGAAAA GAAGACGGAA CATGACGTGT CATCGTCGTG
      ** ** * * * ** * * *   ***   * ** ** *** **
365 :   TTCCACT--G CTGCCACTGT GTCAGG---- ---CTCGG-- --TTAC-TG- CATTTTCTGA

720 :   TGGATCGTCG GACAACAAGG AGAGTATGTT GGTTCCTAGT TCGGCGCGGAG AGAGGATGCA
      ** ***           * * *** ***           ** *   ***** **
410 :   TGAATC---- -----TG A-AGTTTGT- ----- ---GC-ACG TGAGGATACA

780 :   TAGGCCGGAG TTGGAAGAGC GAACAGGATA TTTGGAAATG GATGATCTTT TGGAGATTGA
      *           ** **** *           ** *   *** ** * **
441 :   AA----- -TGCAAGATC ----- --TG G-----TTT TGGTCA--GA

840 :   TGATTTAGGT TTGTTGATTG GCAAAAATGG AGATTTCAAG AATTGGTGTT GTGAAGAGTT
      * * **   ** * * *   *   *****   * * ***   ** **   * ** ***
466 :   T-CTCTA-AC TTCTCGCATT TCCAAAATGT TAAGTCCAAT AACTGCATTG GTTAAG----

900 :   TCAACATCCA TGGAATTGGT TCTGA
      * *   * * **
520 :   ----- TTGGGGCGTT ACTAG

```



Fig. 5-2

0056504

Matching : 36.83 [%]  
Weight : 128

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS -----TKK
  *               ** **** *   *** * *   **** * *
1 : M----- --PSEIVDRK RKSRTGRD-- -VAEILRQWR EYNEQIEAES CIDGGGPKSI

54 : RKVPAKGSKK GCMKGKGGPE NSRCSFRGVR QRIWGKWVAE IREPNGSRL WLGTFTPAQE
  ** * *** * ***** * * **** ** ***** **** * ** ***** *
47 : RKPPPKGSRK GCMKGKGGPE NGICDYRGVR QRRWGKWVAE IREPNGSRL WLGTFTSSSYE

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCV--- HVKTEDPDCE
  ** ***** * ** **** *   * *   * *   * *   * *   * *
107 : AALAYDEAAK AIYQGSARLN LP-----EIT NRSS-STAAAT ATVSGSVTAF SDESEVCARE

171 : SKPFSGGVEP MYCLENAAE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ
  * *   * *   * *   * *   * *   * *   * *   * *
161 : DTNASSG-FG QVKLEDCSDE ---YVLLDSS QCIKEE--- ---LKGKEEV REEHNLA VGF

231 : QQQQDS---- LSVADYGWPN DVDQSHLDSS DMFDVDELLR DLNGDDV--- -FAGLNQDRY
  ***   *   * *   * *   * *   * *   * *   * *
210 : GIGQDSKRET LDAWLMGNGN EQEPLEFGVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH

283 : P-----G NSVANGSYRP -ESQQSGFD- -----PLQS LNYGIPPFQL EGKD---GNG
  *   * *   * *   * *   * *   *   *   *   *   *
270 : PNFSYQTQFP NSNLLGSLNP MEIAQPGVDY GCPYVQPSDM ENYGIDLDRH RFNDLDIQDL

324 : FFDDL SYLDL EN
      *
330 : DFGGDKDVHG ST

```

+++++

Sequence 1 : DREB2A. aa  
Size : 335  
Matching Position : 1 - 335

Sequence 2 : DREB2D. aa  
Size : 206  
Matching Position : 1 - 206

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 28.96 [%]  
Weight : 167

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *               * * *   * *   * *   * *
1 : M----- -SSIE PKVMMVG--- -AN KKQRTVQA-S

61 : SKKGCMKGKG GPENSRCFR GVRQRIWGKW VAEIREPNRG SRLWLGTFT AQAASAYDE
  * **** *** ** * *   ***** ***** ***** *   ***
24 : SRKGCMRGKG GPDNASCTYK GVRQRTWGKW VAEIREPNRG ARLWLGTFT SREAAALAYS

121 : AAKAMYGLA RLNFPRSDAS EVTSTSSQE VCTVETPGCV HVKTEDPDCE SKPFSGGVEP
  ** *** * * * * *   **   **   * * * *

```



Fig. 5-3

0056504

84 : AARKLYGPEA HLNLPESLRS YPKTASS--- PASQTPSSN TGGKSSSDSE S-PCS-----

181 : MYCLENAGEE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ QQQQDSLSVA  
 \* \* \* \* \*

135 : -----SNE M-----S SCGRVTEEIS WEHINV-----DLPVM  
 \* \* \* \* \*

241 : DYGWPNDVDQ SHLDSSDMFD VDELLRDLNG DDVFAGLNQD RYPGNSVANG SYRPESQQSG  
 \* \* \* \* \*

161 : D-----DSS---I WEEATMSLGF PWVHEGDN-----DISR  
 \* \* \* \* \*

301 : FDPLQSLNYG IPPFQLEGKD GNGFFDDLSY LDLEN  
 \*\* \* \* \*

188 : FDTGIS-----GGYSNWDSFH SPL--  
 \* \* \*

+++++

Sequence 1 : DREB2A.aa  
 Size : 335  
 Matching Position : 1 - 335

Sequence 2 : DREB2E.aa  
 Size : 244  
 Matching Position : 1 - 244

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2

Matching : 34.20 [%]  
 Weight : 143

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK  
 \* \* \* \* \*

1 : MEKEDNGSKQ SSSASVSSR ---RRRRVVE PVEATLQRW-----EEEGL ARARRVQAKG  
 \* \* \* \* \*

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGWK VAEIREP---NRGSR LWLGTFTPAQ  
 \*\*\*\*\* \*\* \* \* \*\*\*\*\* \*\* \* \* \*\*\*\*\* \*\*

52 : SKKGCMRGKG GPENPVCFSR GVRQRVWGWK VAEIREPVSH RGANSRSRKR LWLGTFTATA  
 \* \* \* \* \*

113 : EAASAYDEAA KAMYGLARL NFPRSDASEV TSTSSQSEVC TVETPGCVHV KTEDPDCESE  
 \*\*\* \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

112 : EAALAYDRAA SVMYGPYARL NFP-----EDLGGGRK K--DEEAES-  
 \* \* \* \* \*

173 : PFSGGVEPMY CLE-NGAEEM KRGVKADKHW LSEFEHNYWS DILKEKEKQK EQGIVETCQQ  
 \*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

150 : --SGG---Y WLETNKA--- GNGV-----IETEGGK DYVVYNEDAI ELGHDKT-QN  
 \* \* \* \* \*

232 : QQQQDSLSVAD YGWPNDVDQS HLDSSDMFDV DELLRDNLGD DVFAGLNQDR YPGNSVANGS  
 \* \* \* \* \*

191 : PMTDNEIV--NPAVKSE EGYSYDRFKL D-----NGL  
 \* \* \* \* \*

292 : YRPESQQSGF DPLQSLNYGI PPFQLEGKDG NGFFDDLSY- LDLEN  
 \* \* \* \* \*

220 : LYNEPQSS--SYHQC-----GGFD--SYF EYFRF  
 \* \* \* \* \*

+++++

Sequence 1 : DREB2A.aa  
 Size : 335  
 Matching Position : 1 - 335

Fig. 5-4

0056504

Sequence 2 : DREB2F.aa  
 Size : 277  
 Matching Position : 1 - 277

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 27.71 [%]  
 Weight : 176

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : M----- EKSS-----MKQ

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGWK VAEIREPNRG SRLWLGTFPT AQEAASAYDE
    *** ** * * * * * * * * * * * * * * * * * * * * * * * * * *
10 : WKKGPARGKG GPQNALCQYR GVRQRTWGWK VAEIREPKKR ARLWLGSFAT AEEAAMAYDE

121 : AAKAMYGLA RLNFPRSDAS EVTSTS-SQ- ----SEVCT VETPGC---- ----VHVKTE
    ** ** * ** * * * * * * * * * * * * * * * * * * * * *
70 : AALKLYGHDA YLNLPHLQRN TRPSLSNSQR FKWVPSRKF I SMFPSCGMLN VNAQPSVHI I

166 : DPDCESKPFS GGVEPMYCLE NGAEEMKRGV KADKHWLSEF EHNYWSDILK EKEKQKEQGI
    *          *          *          *          *          *          *
130 : QQRLEELKKT GLLSQSYSSS SSSTE----S KTNTSFLDEK TSKGETDNMF EGGDQKKPEI

226 : VETCQQQQQD SLSVADYGWP NDVDQSHLDS SDMFVDVDELL RDLNGDDVFA GLNQDRYPGN
    * ** * * * * * * * * * * * * * * * * *
186 : DLTEFLQLG ILKDENEAEF SEVAECH--S PPPWNEQEET GSPFRTENFS WDTLIEMP--

286 : SVANGSYRPE SQQSGFDPLQ SLNYGIPPFQ LEGKDGNGFF DDLSYLDLEN
    * *          * * * * * * * * * * *
242 : -----RSE TTTMQFD--- SSNFGSYDF- ---EDDVSFP SIWDYYGSLD
  
```

+++++

Sequence 1 : DREB2A.aa  
 Size : 335  
 Matching Position : 1 - 335

Sequence 2 : DREB2G.aa  
 Size : 306  
 Matching Position : 1 - 306

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 26.12 [%]  
 Weight : 184

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : ----- EEEQ PPAKRNMR

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGWK VAEIREPNRG SRLWLGTFPT AQEAASAYDE
  
```

Fig. 5-5

```

                                0056504
15 : * ***** **** * ** ***** **** ***** * *** ****
      SRKGCМКGKG GPENATCTFR GVRQRTWGKW VAEIREPNRG TRLWLGTFNT SVEAAMAYDE

121 : AAKAMYGLA RLN--FPRSD ASEV----TS TSSQSEVCTV ETPGCVHVKT EDPDCESKPF
      *** ** * ** * * * * *
75 : AAKKLYGHEA KLNLVHPQQQ QQVYVNRNLS FSGHSGGSWA YNKKLDMVHG LDLGLGQASC

175 : SGGVEPMYCL ENGAEEMKRG VKADKHWLSE FEHNYWSDIL KEKEKQKEQG IVETCQQQQQ
      * * * * * * * * *
135 : SRG----SCS ERSSFLQEDD DHSHNRCSSS SGSNLCWLLP KQSDSQDQET VNATTSYGGE

235 : DSLSVADYGW PNDVDQSHLD SSDMFDVDEL LRDNGDDVF AGLNQDRYPG NSVANGS---
      * * * * *
191 : GGGGSTLTFS TNLKPNLMS QNYGLYNGAW SRFLVGQEKK TEHDVSSSCG SSDNKESMLV

292 : -----YR PE-SQQSGFD PLQSLNYGIP PFQLEGKDG- --NGFFDDL S YLDLEN
      * ** * * * *
251 : PSCGGERMHR PELEERTGYL EMDDLLEIDD LGLLIGKNGD FKNWCCEEFQ HPWNWF

+++++

Sequence 1      : DREB2A. aa
Size            : 335
Matching Position : 1 - 335

Sequence 2      : DREB2H. aa
Size            : 177
Matching Position : 1 - 177

Matching Condition.

Matches        : -1
Mismatches     : 1
Gaps           : 1
*N+            : 2

Matching       : 28.07 [%]
Weight         : 170

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVE--- ----EVSTKK
  * * * * *
1 : M-----PRK RKSRTGTRD--VAEILRKWR EYNEQTEADS CIDGGGSKPI

54 : RKVPAKGSKK GCMKGKGPE NSRCSFRGVR QRIWGKWVAE IREPNGSRL WLGTFPTAQE
  * * * * *
42 : RKAPPKRSRK GCMKGKGPE NGICDYTGVR QRTWGKWVAE IREPGRGAKL WLGTFSSSYE

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCVHVK TEDPDCESKP
  * * * * *
102 : AALAYDEASK AIYQSARLN LP----- --LLPLC---

174 : FSGGVEPMYC LENGAEEMKR GVKADKHWLS EFEHNYWSDI LKEKEKQKEQ GIVETCQQQQ
  * * * * *
129 : -----QARLL HFLMN---- LK----- -FVHVRIQM

234 : QDSLSVADYG WPNDVDQSHL DSSDMFDVDE LLRDNGDDV FAGLNQDRYP GNSVANGSYR
  * * * * *
150 : DLVL----- --VRSLS RISKMLSPIT AL----- ---VKLGRY-

294 : PESQQSGFDP LQSLNYGIPP FQLEGKDGNG FFDDL SYLDL EN
178 : -----

```

Fig. 5-6

0056504

+++++

Sequence 1 : DREB2B.aa  
 Size : 330  
 Matching Position : 1 - 330

Sequence 2 : DREB2C.aa  
 Size : 341  
 Matching Position : 1 - 341

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 33.62 [%]  
 Weight : 134

```

1 : MAVYEQTGTE QPKKRKSRR AGGLTVADRL KKWKKEYNEIV EASAVKEGEK PK--RKVPAK
  *          ***** * * * * * * * * * * * * * * * *
1 : M-----PSEI VDRKRKSR-- -GTRDVAEIL RQWREYNEQI EAESCIDGGG PKSIRKPPPK

59 : GSKKGCMKGK GGPDNHSCSF RGVQRRIWKG WVAEIREPKI GTRLWLGTFP TAEKAASAYD
  ** ***** * * * * * * * * * * * * * * * *
53 : GSRKGCMKGK GGPENGICDY RGVQRRIWKG WVAEIREPDG GARLWLGTFS SSYEALAYD

119 : EAATAMYGSL ARLNFP---- ------QS VGSEFTSTSS QSEVCTVENK AVVCGDVCVK
  *** * * * * * * * * * * * * * * * *
113 : EAAKAIYGQS ARLNLPEITN RRSSTAATAT VSGSVTAFSD ESEVCAREDT NASSGFGQVK

167 : HEDTDCESNP FSQILDVREE SCG----TRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV
  ** * * * * * * * * * * * * * * * *
173 : LEDCSDEYVL LDSSQCIKEE LKGKEEVREE HNLAVGFGIG QDSKRETLDA WLMGNGNEQE

223 : LQE---KEKP KQEE---EEI QQQQQEQQQQ QLQPDLLTVA DYGPWWSNDI VNDQTSWDPN
  * * * * * * * * * * * * * * * *
233 : PLEFGVDETF DINELLGILN DNNVSGQETM QYQVDRHPNF SYQTQFPN-- SNLLGSLNPM

277 : ECFDINELLG DLNEPGPHQS QDQNHVNSGS YDLHPLHLEP HDGHEFNGLS SLDI
  * * * * * * * * * * * * * * * *
291 : E---IAQPGV DYGCPIYQPS DMENYGIDLD HRRFNDLDIQ DLDFGGDKDV HGST
  
```

+++++

Sequence 1 : DREB2B.aa  
 Size : 330  
 Matching Position : 1 - 330

Sequence 2 : DREB2D.aa  
 Size : 206  
 Matching Position : 1 - 206

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 28.48 [%]  
 Weight : 166

Fig. 5-7

0056504

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  * * * * *
1 : MSSIE----- -PK----- -VMMV GA-----NK KQRTVQA-SS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFTA EKAASAYDEA
    **** * * * * *
25 : KKGCMRGKGG PDNASCTYKG VRQRTWGKVV AEIREPNRGA RLWLGTFTDS REAALAYDSA

121 : ATAMYGSLAR LNFPQSVGSE FTSTSSQSEV CTVENKAVVC GDVCVKHEDT DCESNPFQSI
    * * * * *
85 : ARKLYGPEAH LNLPELSRY PKTASS----- -PASQ-

181 : LDVREESCGT RPDSCVGHG DMNSSLNYDL LLEFEQQYWG QVLQEKEKPK QEEEEIQQQQ
    * * * * *
115 : -----T TPSSNTGG-- -KSSSDSESP CSSNEMSSCG RV----- -TEEI-

241 : QEQQQQQLQP DLLTVADYGW PWSNDIVNDQ TSWDPNECFD INELLGDLNE PGPHQSQQDN
    * * * * *
149 : ----SWEHIN VDLPMDDSS IWEEATMSLG FPWVHEGDND I--SRFDTCI SGGYSNWDSF

301 : HVNSGSYDLH PLHLEPHDGH EFNGLSSLDI
    * * * * *
203 : H----- -SPL-

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

Sequence 2      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

## Matching Condition.

```

Matches          : -1
Mismatched       : 1
Gaps              : 1
* N +            : 2

Matching         : 29.20 [%]
Weight           : 161

```

```

1 : .MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  * * * * *
1 : M-EKEDNG-- --SKQSSA- --SVVSSRRR RRVVEPVEAT LQRWEEGLA RARRVQAKGS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREP----- -KIGTRL WLGTFTA EK
    ***** * * * * *
53 : KKGCMRGKGG PENPVCFRFG VRQVWGKVV AEIREPVSHR GANSSRSKRL WLGTATAAE

113 : AASAYDEAAT AMYGSLARLN FPQSVGSEFT STSSQSEVCT VENKAVVCGD VCVKHEDTDC
    ** *** ** * * * * *
113 : AALAYDRAAS VMYGPYARLN FP-----

173 : ESNPFQILD VREESCGTRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV LQEKEKPKQE
    * * * * *
135 : EDLGGGRKKD EEAESSG--- -GYWL ETNKAGNGVI ETEGKDYVV

233 : EEEIQQQQE QQQQLQPD LTVADYGPW SNDIVNDQTS WDPNECFDIN ELLGDLNEPG

```

Fig. 5-8

0056504

```

176 : YNEDAIELGH DKTQNPMTD- ----- -NEIVNPAVK SEEGYSYDRF KLDNGL----
      *      *      *      *      *      *      *      *
293 : PHQSQQNHV NSGSYDLHPL HLEPHDGHEF -NGLSSLDI
      *      *      *      *      *
220 : -----LYNEP QSSSY----- ----HQGGGF DSYFEYFRF

```

+++++

```

Sequence 1      : DREB2B.aa
Size           : 330
Matching Position : 1 - 330

Sequence 2      : DREB2F.aa
Size           : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 28.06 [%]
Weight       : 163

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  : *----- **
1 : M-----EK ---SSSMKQW

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
    : *** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
11 : KKGPARGKGG PQNALCQYRG VRQRTWGKVV AEIREPKKRA RLWLGSFATA EEAAMAYDEA

121 : ATAMYGSLAR LNFPQSVGSE FTSTS-SQSE VCTVENKAVV CGDVCVKHED TDCESNPFQ
    : * ** * * * * * * * * * * * * * * * * * * * * * * * *
71 : ALKLYGHDAY LNLPHLQRNT RPSLSNSQRF KWVPSRKFI S MFPSCGMLNV NAQPSVHIQ

180 : ILDVREESCG TRPDCTVGH QDMNSSLNYD LLEFEQQYW GQVLQEKEKP KQEEEEIQQ
    : * * * * * * * * * * * * * * * * * * * * * *
131 : QRLEELKKTG LLSQSYSSSS SSTESKTNTS FL--DEKTSK GETDNMFEGG DQKKPEIDLT

240 : QQEQQQQQL- ---QPDLLTV ADYGWPWSND IVNDQTSWDP NECFDINELL GDLNEPGPHQ
    : ** * * * * * * * * * * * * * * * * * * * *
189 : EFLQQLGILK DENEAPSEV AECHSPPWN EQEETGSPFR TENFSWDTLI EMRSETTTM

296 : SQDQNHVNSG SYDLHPLHLE PHDGHEFNGL SSLDI
    : * * * * * * * * * *
249 : QFD--SSNFG SYDFEDDVSF P---SIWYYY GSLD-

```

+++++

```

Sequence 1      : DREB2B.aa
Size           : 330
Matching Position : 1 - 330

Sequence 2      : DREB2G.aa
Size           : 306
Matching Position : 1 - 306

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1

```

Fig. 5-9

0056504

```

Gaps          : 1
*N+           : 2

Matching      : 26.35 [%]
Weight        : 185

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPKGS
   * **
1 : -----EEE QP----- PAKKRNMGRS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKWV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
   ***** * * * *** **** * * * * * * * * * * * * * * * *
16 : RKGCMKGKGG PENATCTFRG VRQRTWGKWV AEIREPNRGT RLWLGTFNTS VEAAMAYDEA

121 : ATAMYGLSLAR LN--FPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCESNPFS
   * ** * ** * * * * * * * * * * * * * * * *
76 : AKKLYGHEAK LNLVHPQQQQ QVVVNRNLSF SGHSGSGWAY NKKLDMVHGL DLGLGQASCS

179 : QILDVREESC GTRPDSCTVG HQDMNSSLNY DLLLEFEQQY WGQVLQEKEK PKQEEEEIQQ
   * * * * * * * * * * * * * * * *
136 : -RGSCSERSS FLQED-DDHS HNRCSSSSGS NLCWLLPKQS DSQDQETVNA TTSYGEGGG

239 : QQEQQQQQQL QPDLLTVADY G---WPWS-- -----N DIVNDQTSWD PNECFDINEL
   * * * * * * * * * * * * * * * *
194 : GSTLTFSTNL KPNLMSQNY GLYNGAWSRF LVGQEKKTEH DVSSSCGSSD NKESMLVPSC

285 : LG---DLNEP GPHQSQQDNH VNSGSYDLHP LHLEPHD--- -GHEFNGLSS LDI
   * * * * * * * * * * * *
254 : GGERMHRPEL EERTGYLEMD DLLEIDDLGL LIGKNGDFKN WCCEEFQHPW NWF

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

```

```

Sequence 2      : DREB2H.aa
Size            : 177
Matching Position : 1 - 177

```

Matching Condition.

```

Matches         : -1
Mismatches      : 1
Gaps            : 1
*N+             : 2

Matching        : 28.92 [%]
Weight          : 160

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EA--SAVKEG EKP RKVPK
   * * * * * * * * * * * * * * * *
1 : M----- -PRKRKSR-- -GTRDVAEIL RKWREYNEQT EADSCIDGGG SKPIRKAPK

59 : GSKKGCMKGK GGPDSHCSF RGVRQRIWGK WVAEIREPKI GTRLWLGTFP TAEKAASAYD
   * * * * * * * * * * * * * * * *
48 : RSRKGCMKGK GGPENGICDY TGVRQRTWGK WVAEIREPGR GAKLWLGTF S SYEAALAYD

119 : EAATAMYGLSL ARLNFPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCESNPFS
   * * * * * * * * *
108 : EASKAIYGQS ARLNLP-----

```

Fig. 5-10

0056504

```

179 : QILDVREESC GTRPDSCTVG HQDMNSSLNY DLLLEFEQQY WGQVLQEKEK PKQEEEEIQQ
124 : ----- --LLPLCQ-- -ARLLHFLMN LKFVHVRIQM

239 : QQEQQQQQQL QPDLLTVADY GWPWSNDIVN DQTSWDPNEC FDINELLGDL NEPGPHQSQD
    *      **      *      *      *      *
149 : Q----- --DL----- --VLVR SLTS----- -RISKML--- -----SPI

299 : QNHVNSGSYD LHPLHLEPHD GHEFNGLSSL DI.
    * * *
169 : TALVKLGRY- -----

```

+++++

```

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341

```

```

Sequence 2      : DREB2D.aa
Size            : 206
Matching Position : 1 - 206

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 29.03 [%]
Weight           : 167

```

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
  * *      * *      * *      * *      * *      * *
1 : MSS----- -IEPKVMMVG ANKK--QRTV QASSRKGCMR

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLTG FSSSYEAALA YDEAAKAIYG
    ***** * * * ***** * ***** * * ***** ** ** **
31 : GKGGPDNASC TYKGVQRRTW GKWVAEIREP NRGARLWLTG FDTSSREAALA YDSAARKLYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDSCSDEY
    * *****      * * * *      * * * *      * *
91 : PEAHLNLPE- ----- SLRSYPKTAS SPAS----- QTPSSNTG- --GKSSSD--

181 : VLLDSSQCIK EELKGKEEVR EEHNLAVGFG IGQDSKRETL DAWLMGNGNE QEPLEFGVDE
    * *      * *      * *
129 : ---SESPCSS NEMSSCGRVT EE----- -----IS

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG
    ** *      *      *      *      *
150 : WEHINVDPV MDDSSIWEEA TM----- --SL-----G

301 : CPYVQPSDME NYGIDLHRR FNDLDIQDLD FGGDKDVHGS T
    * *      * * * * * *      * *
175 : FPWV----- -HEGDNDISR F-DTCISGGY SNWD-SFHSP L

```

+++++

```

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341

```



Fig. 5-11

Sequence 2 : DREB2E.aa  
Size : 244  
Matching Position : 1 - 244

0056504

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 30.29 [%]  
Weight : 172

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEA-ESCID GGGPKSIRKP PPKGSRKGCM  
\* \* \* \* \*  
1 : MEKEDNGSKQ SS---SASVV SSRRRRRVVE PVEATLQRWE EEGLARARRV QAKGSKKGCM  
  
60 : KGKGGPENGI CDYRGVRQRR WGKWVAEIRE P--DGGA--- ---RLWLGTF SSSYEALAY  
\*\*\*\*\* \* \*\*\*\*\* \*  
58 : RGKGGPENPV CRFRGVRQRV WGKWVAEIRE PVSHRGANSS RSKRLWLGTF ATAAEALAY  
  
112 : DEAAKAIYGQ SARLNLPEIT NRSSSTAATA TVSGSVTAFS DESEVCARED TNASSGFGQV  
\* \* \* \* \*  
118 : DRAASVMYGP YARLNFPE-- ----- -DLGGGRKKD EEAE----- -SSG-----  
  
172 : KLEDCSDEYV LLDSSQCIKE ELKGKEEVRE EHNLA VGFGI GQDSKRETLD AWLMGNGNEQ  
\* \* \* \* \*  
152 : -----GYW L----- ETNKA---GN G---VIETEG GKDYVVYNE-  
  
232 : EPLEFGVDET FDINELLGIL NDNVSGQET MQYQVDRHPN FSYQTQFPNS NLLGSLNPME  
\* \* \* \* \*  
179 : DAIELGHDKT QNPMTDNEIV NPAVK---E EGYSYDR--- -----FKLD N-----  
  
292 : IAQPGVDYGC PYVQPSDMEN YGIDLHRRF NOLDIQDLDF GGDKDVHGST  
\* \* \* \* \*  
218 : ----GLLYNE P--QSSSYHQ GG----- --GFDSYF ----EYFRF

+++++

Sequence 1 : DREB2C.aa  
Size : 341  
Matching Position : 1 - 341

Sequence 2 : DREB2F.aa  
Size : 277  
Matching Position : 1 - 277

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 29.89 [%]  
Weight : 172

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PPKGSRKGCMK  
\* \* \* \* \*  
1 : M----- --EKS---SS MKQWKGPAP  
  
61 : KGKGGPENGI CDYRGVRQRRW GKWVAEIREP DGGARLWLGTF FSSSYEALAY DEAAKAIYG  
\*\*\*\*\* \* \*\*\*\*\* \* \*\*\*\*\* \* \* \* \* \*

Fig. 5-12

```

                                0056504
17 : GKGGPQNALC QYRGVRQRTW GKWVAEIREP KKRARLWLGS FATAEEAAMA YDEAALKLYG

121 : QSARLNLP-- -EITNRSSST AATATVSGSV TAFSDESEVC AREDTNA--S SGFGQVKLED
      * ***      * * *      * *      * * *      * * *
77 : HDAYLNPLHL QRNTRPSLSN SQRFKWVPS- RKFISMFPSC GMLNVNAQPS VHIIQQRLE-

176 : CSDEYVLLDS SQCIKEELKG KEEVREEHNL AVFGGIGQDS KRETLDALWM GNGNEQEPL
      ** **      * *      * * *      * * *      * * *
135 : ELKKTGLL-- SQ-----SYS SSSSSTESKT NTSFLDEKTS KGET---DNM FEGGDQKKPE

236 : FGVDETFDIN ELLGILNDNN VSGQETMQYQ V-DRHPNFSY QTQFPNSNLL GSLNPMEIAQ
      * *      **** * *      * *      * *      * *
185 : --IDLT-EFL QQLGILKDEN ----EAEPSE VAECHSPPPW NEQ----EET GSPFRTENFS

295 : PGVDYGCPIYV QPSDMENYGI DLDHRRFNDL DIQDLDFGGD KDVHGS-T
      * *      * *      * *      * *      * *
234 : WDTLIEMPRS ETTMQFDSS NFGSYDFED- ---DVSFPSI WDYYGSLD

++++++

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306

Matching Condition.

Matches        : -1
Mismatch       : 1
Gaps           : 1
* N+           : 2

Matching       : 28.25 [%]
Weight        : 174

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCМК
1 : -----EEE QPPA-----KKNR MGRSRKGCМК

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
      * * * * * * * * * * * * * * * * * * * * * * * *
22 : GKGGPENATC TFRGVRQRTW GKWVAEIREP NRGTRLWLGT FNTSVEAAMA YDEAAKKLYG

121 : QSARLNLP-- -PEITNR SSSTAATATV SGSVTAFSDE SEVCAREDTN ASSGFGQVKL
      * * *      * *      * *      * *      * *
82 : HEAKLNLVHP QQQQVVVNR NLSFSGHSG SWAYNKKLDM VHGLDLGLGQ ASCSRG-SCS

174 : EDCSDEYVLL DSSQCIKEEL KGKEEVREEH NLAVFGGIGQ DS-KRETLD --WLMGNGNE
      * *      * *      * *      * *      * *      * *
141 : ERSSFLQEDD DHSHNRCSSS SG-----S NLCWLLPKQS DSQDQETVNA TTSYGGEQGG

231 : QEPLEF-GVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH PNFSYQTQFP N--SNLLGSL
      * *      * *      * *      * *      * *      * *
194 : GSTLTFSTNL KPNLMSQNY GLYNGAWSRF LVGQEKKTEH DVSSSCGSSD NKESMLVPSC

288 : NPMEIAQPGV DYGCPIYVQS DMENYIDLD HRRFNDLDIQ DLDFGGDKDV HGST
      * *      * *      * *      * *
254 : GGERMHRPEL EERTGY-LEM DDLLEIDDLG LLIKNGDFK NWCCEEFQHP WNW

```

Fig. 5-13

0056504

+++++

Sequence 1 : DREB2C.aa  
 Size : 341  
 Matching Position : 1 - 341

Sequence 2 : DREB2H.aa  
 Size : 177  
 Matching Position : 1 - 177

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 38.42 [%]  
 Weight : 97

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCМК  
 \*\* \*\*\* \*\*\*\*\* \*\* \* \* \* \* \*  
 1 : MP-----RKR KSRGTRDVAE ILRKWREYNE QTEADSCIDG GGSKPIRKAP PKRSRKGCМК

61 : GKGGPENGIC DYRGVRQRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG  
 \*\*\*\*\* \*\* \* \* \* \* \*  
 56 : GKGGPENGIC DYTGVQRQW GKWVAEIREP GRGAKLWLGT FSSSYEAALA YDEASKAIYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDCSDEY  
 \*\*\*\*\*  
 116 : QSARLNLP-----

181 : VLLDSSQCIK EELKGKEEVR EEHNLAVGFG IGQDSKRETL DAWLMGNGNE QEPLEFGVDE  
 \*\* \* \* \* \* \*  
 124 : -LLPLCQ----- -ARL----- -LHF-----

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG  
 \* \* \* \* \*  
 136 : -----LMN LKFVHVRIQ- -MQDLV----- -LVRSL-----

301 : CPYVQPSDME NYGIDLHRR FNDLDIQDLD FGGDKDVHGS T  
 \* \* \* \* \*  
 158 : --TSRISKM- -----LS PITALVKLGR Y

+++++

Sequence 1 : DREB2D.aa  
 Size : 206  
 Matching Position : 1 - 206

Sequence 2 : DREB2E.aa  
 Size : 244  
 Matching Position : 1 - 244

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 35.20 [%]  
 Weight : 96

Fig. 5-14

0056504

```

1 : M-----SS- -IEPKVMMVG A----- NKKQRTVQA- SSRKGCMRGK
   *      **      * * *      * * * *
1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK

33 : GGPDNASCY KGVQRQWVGK WVAEIREP-- NRG----- RLWLGTFDTS REAALAYDSA
   * * * * * * * * * * * * * * * * * * * *
61 : GGPENPVCRF RGVQRVWVGK WVAEIREPVS HRGANSRSRK RLWLGTFATA AEAALAYDRA

85 : ARKLYGPEAH LNPESLSY PKTASSPASQ TTPSSNTGCK SSSDSESPCS SNEMSSCGRV
   * * * * * * * * * * * * * * * * * * * *
121 : ASVMYGPYAR LNPEDLGGG RKKDEEAESS GGYWLETNKA GNGVIE---- -TEGGKDYVV

145 : TEE--ISWEH INVDPVMD SSIWEEATMS --LGFVWVHE GDNDISRFDT CIS----GGY
   * * * * * * * * * * * * * * * * * * * *
176 : YNEDAIELGH DKTQNP-MTD NEIVNPAVKS EEGYSYDRFK LDNGLLYNEP QSSSYHQGGG

197 : SNWDSFHSPL

235 : FDSYFEYFRF

```

+++++

```

Sequence 1      : DREB2D.aa
Size            : 206
Matching Position : 1 - 206

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*#+              : 2

Matching          : 32.65 [%]
Weight            : 129

```

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGVQRQWV GKWVAEIREP
   * * * * * * * * * * * * * * * * * * * *
1 : M---EKSSSM ----KQ--- ---WKKGPAR GKGGPQNALC QYRGVQRQWV GKWVAEIREP

61 : NRGARLWLGT FDSREAALA YDSAARKLYG PEHLNLP-- ----ESL-- ----RSYP
   * * * * * * * * * * * * * * * * * * * *
47 : KKRARLWLGS FATAEEAAMA YDEAALKLYG HDAYLNLP HL QRNTRPSLSN SQRFKWVPSR

106 : KTASSPAS-- ----QTPS- ----- SNTGGKS--- SSDSESPCS- ----SNEMS
   * * * * * * * * * * * * * * * * * * * *
107 : KFISMFPSCG MLNVNAQPSV HIIQRLEEL KKTGLLSQSY SSSSSSTESK TNSFLDEKT

140 : -----SC G-----R VTEEISWEH I NVDPVMD SSIWE----- --EATMSL
   * * * * * * * * * * * * * * * * * * * *
167 : SKGETDNMFE GGDQKKPEID LTFELQLGI LKDENEAEPS EVAECHSPPP WNEQEETGSP

174 : GFPVWHEGDN DI----- -SRFDTCSG GY----- -SNWDSFHSP L
   * * * * * * * * * * * * * * * * * * * *
227 : FRTENFSWDT LIEMPRSETT TMQFDSSNFG SYDFEDDVSF PSIDWYCGSL D

```

+++++

Fig. 5-15

0056504

Sequence 1 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Sequence 2 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 32.08 [%]  
Weight : 144

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGYRQRTW GKWVAEIREP
    *      **      *****      * * *      * * *      * * *      * * *
1 : EEQPP-----AKK--RN MGRSRKGCMK GKGGPENATC TFRGVRQRTW GKWVAEIREP

61 : NRGARLWLG FDSREAALA YDSAARKLYG PEHLNL-----
    ***      * * *      * * *      * * *      * * *
52 : NRGTRLWLG FNTSVEAAMA YDEAAKLYG HEAKLNLVHP QQQQVVVNR NLSFSGHGSG

98 : -----PESLRSYPKT AS-SPASQTT PSS-----NTGGKSS-----
    *      * * *      * * *      * *
112 : SWAYNKKLDM VHGLDLGLGQ ASCSRGSCSE RSSFLQEDDD HSHNRCSSSS GSNLCWLLPK

127 : -SDS-----ES PCSS-----NEMS-----S CGRVTEEISW
    ***      *      *      * * *      * * *
172 : QSDSQDQETV NATTSYGEG GGGSTLTFT NLKPKNLMSQ NYGLYGAWS RFLVGQEKKT

151 : EHINVLPYM DDSSIWEE--ATMSLGFPPV H-----EGD-----N DISRFDTGIS
    ** *      ** *      * * *      * * *      * *
232 : EH--DVSSS CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDDLLEI DDLGLLIGKN

194 : GGYSNW--DS FHSP---L
    * * *      *
289 : GDFKNWCCEE FQHPWNWF
  
```

+++++

Sequence 1 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 32.03 [%]  
Weight : 101

```

1 : M-----SSIEPK-----VMMVGANKK QR-TVQASSR KGCMRGKGGP
    *      * *      * * *      * * *      * * *
1 : MPRKRKSRGT RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCMKGKGGP
  
```

Fig. 5-16

0056504

```

36 : DNASCTYKGV RQRTWGKWVA EIREPNRGAR LWLGTFTSR EAALAYDSAA RKLYGPEAHL
    * * * * * ***** * * * * *
61 : ENGICDYTG V RQRTWGKWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYGQSARL

-96 : NLPESLRYP KTASSPASQT TPSSNTGGKS SSDSESPCSS NEMSSCGRVT EEISWEHINV
    ** * * * * *
121 : NL-----P LLPLCQARLL HFLMN--LKF VHVRIQMQL VLVRS---LT SRIS-----

156 : DLPVMDSSI WEEATMSLGF PWVHEGDNDI SRFDTCSGG YSNWDSFHSP L
    * * * * *
163 : ----KMLSPI --TALVKLG- -----R Y

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

```

```

Matching         : 27.52 [%]
Weight           : 173

```

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
    ***      ***
1 : MEK----- SSS-----MK QWKKGPARGK

61 : GGPENPVCRF RGVQRVWVGK WVAEIREPVS HRGANSSRSK RLWLGTFFATA AEAALAYDRA
    *** * * ***** * * * * *
19 : GGPQNALCQY RGVQRVWVGK WVAEIREP-- ----KKRA RLWLGSFATA EEAAMAYDEA

121 : ASVMYGPYAR LN-----FP-----
    * ** * **
71 : ALKLYGHDAY LNLPHLQNT RPSLSNSQRF KWVPSRKFI S MFPSCGMLNV NAQPSVHIQ

135 : ----EDLGGG RKKDEEAESS GGYWLETN-- ----KAGN GVIETEGG-- -KDYVVVYNED
    * * * * *
131 : QRLEELKKTG LLSQSYSSSS SSTESKTNTS FLDEKTSKGE TDNMFEGGDQ KKPEIDLTEF

180 : AIELGHDKTQ N---PMTDNE --IVNPAVKS EEGYSYDR-F KLDNGLLYNE PQS-----
    ** * * * * *
191 : LQLGLILKDE NEAEPSEVAE CHSPPPWNEQ EETGSPFRTE NFSWDTLIEM PRSETTTMQF

227 : -SSYHQGGGF --DSYF---- --EYFRF
    ** * *
251 : DSSNFGSYDF EDDVSFPSIW DYYGSLD

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244

```

Fig. 5-17

0056504

Matching Position : 1 - 244

Sequence 2 : DREB2G.aa  
 Size : 306  
 Matching Position : 1 - 306

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 25.07 [%]  
 Weight : 197

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGC MRGK
1 : ----- ** * * **** **
61 : GGPENPVC RF RGVQRVWGK WVAEIREPVS HRGANSSRSK RLWLGT FATA AEAALAYDRA
24 : GGPENATCTF RGVQRRTWGK WVAEIREP-- ----NRGT RLWLGT FNTS VEAAMAYDEA
121 : ASVMYGPYAR LN----- ----FPE DLGG-----
76 : AKKLYGHEAK LNLVHPQQQQ QVVVNRNLSF SGHSGSWAY NKKLDMVHGL DLGLGQASCS
141 : RKKDEEAES- ----SGG YWL----- --ETNKA-- ----GNGV
136 : RGSCSERSSF LQEDDDHSHN RCSSSSGSNL CWLLPKQSDS QDQETVNATT SYGGE GGGGS
165 : IET----- --EGGKDYVV YN----- EDAIELGHDK TQNPMTDNEI VNPVKSEEG
196 : TLTFTSNLKP KNLM SQNYGL YNGAWSRFLV GQEKTEHDV SSSCGSSDNK ESMLVPSCGG
208 : YSYDRFKL-- ----DNG LLYNEPQSSS YHQGGGFDSY FEYF-----R F
256 : ERMHRPELEE RTGYLEMDDL LEIDDLGLLI GKNGDFKNWC CEEFQHPWNW F

```

+++++

Sequence 1 : DREB2E.aa  
 Size : 244  
 Matching Position : 1 - 244

Sequence 2 : DREB2H.aa  
 Size : 177  
 Matching Position : 1 - 177

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 29.92 [%]  
 Weight : 114

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGC MRGK
1 : MPRKRKSRGT RDVA--EILR KWREYNEQTE A-DSCIDGGG SKPIRKAPPK RSRKGC MKGK

```

Fig. 5-18

```

                                0056504
61 : GGPENPVCRF RGVQRVWGK WVAEIREPVS HRGANSSRSK RLWLGTFATA AEAALAYDRA
    ***** * ***** *** ***** *** ***** ***** *
58 : GGPENGICDY TGVQRRTWGK WVAEIREP-- GRGA----- KLWLGTFSSS YEAALAYDEA

121 : ASVMYGPYAR LNFPELGGG RKKDEEAESS GGYWLETNKA GNGVIETEGG KDYVVYNEDA
    ** ** * * * * * * * * * * * * * * * *
110 : SKAIYGQSAR LNLP-LLPLC QAR----- ---LLHFLMN LKFVHVRIQM QDLV-----

181 : IELGHDKTQN PMTDNEIVNP AVKSEEGYSY DRFKLDNGLL YNEPQSSSYH QGGGFDSYFE
    * * * * * * * * * * * * * * * *
153 : --LVRSLTSR ISKMLSPITA LVK----- -----

241 : YFRF
    *
174 : LGRY

```

+++++

```

Sequence 1      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

```

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 31.41 [%]
Weight           : 138

```

```

1 : ME-----KSS SMKQWKKGPA RKGKGPQNAL CQYRGVRQRT WGWVVAEIRE PKKRARLWLG
  * * * * * * * * * * * * * * * * * * * *
1 : EEEQPPAKKR NMGRSRKGCN KGKGGPENAT CTFRGVRQRT WGWVVAEIRE PNRGTRLWLG

56 : SFATAEEAAM AYDEAALKLY GHDAYLNLPH LQ-----RN TRPSLSNSQR FKWVPSRKFI
  * * * * * * * * * * * * * * * * * * * *
61 : TFNTSVEAAM AYDEAAKLY GHEAKLNLVH PQQQQQVVVN RNLSFSGHGS GSW-AYNKKL

110 : SMFPSCGMLN VNAQPSVHII QQRLEELKKT GLLSQSYSSS SS-----STE SKTNTSFLDE
  * * * * * * * * * * * * * * * * * * * *
120 : DMVHGLDLGL GQASCSRGSC SERSSFLQED DDHSHNRCSS SSGSNLCWLL PKQSDS-QDQ

165 : KTSKGETDNM FEGG----- --DQKKP--- ---EIDLTEF LQQLGILKDE NEAEPSEVAE
  * * * * * * * * * * * * * * * * * * * *
179 : ETVNATTSYG GEGGGGSTLT FSTNLKPKNL MSQNYGLYNG AWSRFLVGQE KKEHDVSSS

211 : CHS---PPPWN EQEETGS--P FRTENFSWDI LIEM-PRSET TTMQFDSSNF GSYDFEDDVS
  * * * * * * * * * * * * * * * * * * * *
239 : CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDLLEI DDLGLLIGKN GDFKNWCCEE

266 : FPSIWYYGS LD
  * *
299 : FQHPW----N WF

```

+++++



Fig. 5-19

0056504

Sequence 1 : DREB2F.aa  
Size : 277  
Matching Position : 1 - 277

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 21.52 [%]  
Weight : 192

```

1 : M---EKS--- -----SSMKQWK KGPARGKGGP
   *  **
1 : MPRKRKSRGT RDVAEILRWK REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCМКGKGGP

22 : QNALCQYRGV RQRTWGKWVA EIREPKKRAR LWLGSFATAE EAAMAYDEAA LKLYGHDAYL
    * * * * *
61 : ENGICDYTGВ RQRTWGKWVA EIREPGRGAK LWLGTFSSTY EAALAYDEAS KAIYQGSARL

82 : NLPHLQRNTR PSLSNSQRFK WVPSRKFISM FPSCGMLNVN AQPSTVHIQQ RLEELKKTGL
    *** * * * *
121 : NLPLLPLCQA RLLHFLMLNK FV-----HVRIQMQ DL-----V

142 : LSQSYSSSSS STESKTNTSF LDEKTSKGET DNMFEГGDQK KPEIDLTEFL QQLGILKDEN
    * * * * *
153 : LVRSLSRIS KMLS-----PITAL VKLG-----

202 : EAEPSEVAEC HSPPPWNEQE ETGSPFRTEH FSWDTLIEMP RSETTTMQFD SSNFGSYDFE
176 : -----

262 : DDVSFPSIWD YYGSLD
176 : -----RY
  
```

+++++

Sequence 1 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 24.41 [%]  
Weight : 192

Fig. 5-20

```

                                0056504
1 : -----EEEQ-----PP AKKRNMGSR KGCМКGKG GP
    ** * * *** *****
1 : MPRKRKSRGT RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCМКGKG GP

27 : ENATCTFRGV RQRTWGKWVA EIREPNRGTR LWLGTFTSV EAAMAYDEAA KKLYGHEAKL
    ** * ** ***** ** ***** * *** ***** * ** *
61 : ENGICDYTG V RQRTWGKWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYGQSARL

87 : NLVHPQQQQ VVVNRNLSFS GHGSGSWAYN KKLDMVHGLD LGLGQASCSR GSCSERSSFL
    ** * *
121 : NL-----PL LPLCQA-----

147 : QEDDDHSHNR C SSSSGSNLC WLLPKQSDSQ DQETVNATTS YGGEGGGGST LTFSTNLKPK
    * * ***
131 : -----RL LHFLMNLKFV

207 : NLMSQNYGLY NGAWSRFLVG QEKKTEHDVS SSCGSSDNKE SMLVPSCGGE RMHRPELEER
    * * ** * * * ** *
143 : HVRIQMDL- -----VLV- -----RSLTSRISK- -MLSP-----

267 : TGYLEMDDL EIDDLGLLIG KNGDFKNWCC EEFQHPWNWF
    * * *
168 : -----ITALVKL-----GRY

```

Fig. 6

DREB1C.nuc 1: ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGCTCTCCGTTTCCTCGGCCGGTGGATTACA  
DREB1D.nuc 1: ATGAATCCATTTTACTCTACATTCCTCAGACTCGTTTCTCTCAATCTCCGATCATAGATCTCCGTTTCAGACAATACTAGTGTGT  
DREB1A.nuc 1: ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGCTCTCCGTTTCCTCGGCCGGTGGATTACA  
DREB1B.nuc 1: ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGCTCTCCGTTTCCTCGGCCGGTGGATTACA  
DREB1E.nuc 1: .....GGCTCCGATTACGAGCTCTCCGTTTCCTCGGCCGGTGGATTACA  
DREB1F.nuc 1: .....ATGCAAAACGAGC  
.....ATGAAATAATGATG

DREB1C.nuc 77: GTCGGAAGCTTGCCACGAGCTGCCCGAGAAACACGCGGAAGGAAGAAGTTTCGTGAGNCTCGTCACCCCAATTACAGAGGAGT  
DREB1D.nuc 86: CACCAAGAGTTAGCTTCACAGTCTCCAAAGAAACGAGCTGGGAGGAAGAAGTTTCGTGAGNCTCGTCACCCCAATTACAGAGGAGT  
DREB1A.nuc 77: TCCGACCGCTTCGAGCAGCTGCCCGAGAAACGCGCGGGTCTAAGAAGTTTCGTGAGNCTCGTCACCCCAATTACAGAGGAGT  
DREB1B.nuc 68: GTCGACCGTTGGCCACGAGTTGTCCGAGAAACGCGCGGGTCTAAGAAGTTTCGTGAGNCTCGTCACCCCAATTACAGAGGAGT  
DREB1E.nuc 14: ATATCACCGTGGCCGAGATGAAGCCAAAGAAGCTGCTGGACGGAGGATTTTCAAGGAGACAAGTCACCCCAATTACAGAGGAGT  
DREB1F.nuc 14: ATATTATTCTGGCGGAGATGAGGCTTAAGAAGCTGCGGGAGGAGAGTGTTTAAGGAGACAAGTCACCCCAATTACAGAGGAGT

DREB1C.nuc 162: TCGTCAGAGAACTCCGGTAAAGTGGTGTGTGAGTTGAGAGGSCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACC  
DREB1D.nuc 171: TCGTCAGAGAACTCCGGTAAAGTGGTGTGTGAGTTGAGAGGSCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACC  
DREB1A.nuc 162: TCGTCAGAGAACTCCGGTAAAGTGGTGTGTGAGTTGAGAGGSCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACC  
DREB1B.nuc 153: TCGTCAGAGAACTCCGGTAAAGTGGTGTGTGAGTTGAGAGGSCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACC  
DREB1E.nuc 99: GCGGCTAGCGGACGGCCACAAATGGGTCTCCGAAGTCAGAGAACCGACGCAACACGCCCTATTGGCTCGGGACTTTCCAAACC  
DREB1F.nuc 99: AAGCGGAGGACGGTGAACAATGGGTCTCCGAAGTCAGAGAACCGACGCAACACGCCCTATTGGCTCGGGACTTTCCAAACC

DREB1C.nuc 247: GCTGAGATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGCAATCTGCTGTCTCAATTTCCGTGACTCGGGCTT  
DREB1D.nuc 256: GTTGAATATGGCTGCTCTGCTCATGATGTTGCTGCTTAGCTCTCGTGGTCTGCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1A.nuc 247: GCTGAGATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1B.nuc 238: GCTGAGATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1E.nuc 184: GCAGATATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1F.nuc 184: GCAGATATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTGCTCTCAATTTCCGTGACTCGGGCTT

DREB1C.nuc 332: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG  
DREB1D.nuc 341: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG  
DREB1A.nuc 332: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG  
DREB1B.nuc 323: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG  
DREB1E.nuc 269: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG  
DREB1F.nuc 269: GCGGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGGCTGAAGCCGCGTTGAATTTTCAA...GATGAG

DREB1C.nuc 415: AT...GTGTCTATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1D.nuc 424: ATACGACGAGGAGGATCTAAACTGCGGCGGAGGCGAGAGGAGGCGGAGGGGAGGG...GTGAGGGAGGGGAG...AGGAGGG  
DREB1A.nuc 415: AT...GTGTCTATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1B.nuc 406: AC...GTGTCTATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1E.nuc 354: GTT...AGTACAGGAATTACGTTTACCTCAGCCAGTGA...TTTACACG...TTTACACG  
DREB1F.nuc 354: TTTA...GAAAGTGGAATTACGTTTACCTCAGCCAGTGA...TTTACACG...TTTACACG

DREB1C.nuc 482: CGCCGGAAC...AGAGCCAGATGCGTTTATATGGATGAAGAGGCGATGTTGGGATGCTCTAGTTTGTGGATAACATGGCCG  
DREB1D.nuc 503: CGGAGGAGC...AGAATGCTGCTGTTTATATGGATGAAGAGGCGATGTTGGGATGCTCTAGTTTGTGGATAACATGGCCG  
DREB1A.nuc 479: CGGAGGAGC...AGAGCCAGATGCGTTTATATGGATGAAGAGGCGATGTTGGGATGCTCTAGTTTGTGGATAACATGGCCG  
DREB1B.nuc 473: CGCCGGAAC...AGAGCCAGATGCGTTTATATGGATGAAGAGGCGATGTTGGGATGCTCTAGTTTGTGGATAACATGGCCG  
DREB1E.nuc 402: TCGG...ATGAAGGAGTCCGTGGAATGATGATGAGGCTCGCGG  
DREB1F.nuc 431: GTTCCGGATCGGAGGAGAGGATCTCTCTCTCGTATGGATTTGAGACTACCAAGAGTCTCAGCGACCAATGATGAGACTCGCGG

DREB1C.nuc 563: AAGGGATGCTTTTACCGTCCGC...GTCGGTCAATGGAACTATAATT...TTGATGTCGAGGGGAGA...TGATGA  
DREB1D.nuc 584: AAGGGATGCTTTTACCGTCCGC...GGAAGTGGCTGGAATCATAAC...GACTTTGACGGAGT...GGGTGA  
DREB1A.nuc 560: AAGGGATGCTTTTACCGTCCGC...GTCCCTACAGTGGAAATCATAATC...ATGAAGTCCAGCCGCA...TGATGA  
DREB1B.nuc 554: AAGGGATGCTTTTACCGTCCGC...GTCTGTCAATGGAAATCATAAT...ATGAGTCCAGCCGCA...TGATGA  
DREB1E.nuc 443: AAGGACCGCTTGGATGTCGCGCCCAAGATCGTACATGA...TATGAAT...ACGAGTGTGTACGTTGGACGAGAAATGTGTACGA  
DREB1F.nuc 515: AGGGCCACTAATGTCGCGCCCGGATCGTATATGGAGAGCATGACCTCTACTAATGTTTACAGGAGAGAGATGTGTATGA

DREB1C.nuc 630: CG...TGTCCTTATGGAGCTATTA...  
DREB1D.nuc 648: CG...TGTCCTTATGGAGCTATTA...  
DREB1A.nuc 627: CGGCGTATCGTTATGGAGTTATTA...  
DREB1B.nuc 621: CG...TGTCCTTATGGAGTTATTA...  
DREB1E.nuc 522: AGATTGTCTACTTGGAGTTATTA...  
DREB1F.nuc 600: AGATATGTCATGTTGGAGTTACAGATATTA

DREB2A.nuc  
DREB2B.nuc  
DREB2C.nuc  
DREB2H.nuc  
DREB2E.nuc  
DREB2D.nuc  
DREB2G.nuc  
DREB2F.nuc

:ATGCCAGTTTATGATCAGAGTGGAGATAGAAACAGACAACAAATTGTATACATCTCGAGGATATGGGAAATCTAAGATGAGGGTGACG  
 :.....ATGCGTGT.ATATGACAAACCG.GAACCGAGACCGGAATGAATGGAAATCTAAGGCGTCCGAGCAGAGTGC  
 :.....ATGCCGTGGGAGATTGTGACAGGAAAGGAAATGATCTC.....TGGACACACGAG  
 :.....ATGCCCAGGAAAGCGGAAATCTC.....TGGACACACGAG  
 :.....ATGGAAGGGAGTAAACGGATCGAATACACAG

DREB2A.nuc .. ACTGCGCTGAGAGATTAAGAGAGATGGAAACAGATATACG...ACCGTAGAG...AAGTTTCTACCAAGAA  
 DREB2B.nuc ..TTTA..ACGAGGCTGATAGCTTAAAGATGCCAAGGTATACACG...ATTGTCAGCTC...GGCTGTAAAGCAAGGA  
 50AA...GAACTGAGATCTTAAGGACATGAGAGATGACAGAGATACGAGATC...TTGTACCGATGCTGGT  
 35AA...GAACTGAGATCTTAAGGACATGAGAGATGACAGAGATACGAGATC...TTGTACCGATGCTGGT  
 33CCCTCTGCTTCCTGTTGATCTCTCGAGAGACGAGAGAGATGGTGGACCCAGCTGAAACGACGTACAGAGATGGGAGAGCTTA  
 1:.....ATGTATCTCATGAGCCATAGTAATGA...TGGTGGGTGCTTAATAT...ATGGAAGAA  
 DREB2G.nuc .....  
 DREB2F.nuc .....

159 **GA** .. **GGAA** ..... **AGTAACTCGAAGAAGCGTCGAA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
145 **CA** .. **GAAA** **CGGAAACGGTAAAGT** **CCTGCAAAAGC** **TGCA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
124 **GGTCCAAA** **TGAT** **ATGCGCCCTCC** **TAAAGCTTCGAA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
109 **GGTCCAAA** **CAAT** **TCGAAAGCTTCGAA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
118 **GATTGGCGA** **AGCTCT** **GTGCTCAAGT** **CGCAAGCTTCGAA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
45 **GA** .. **ACCA** **CGAAGCAACCC** ... **GTCCCAAGT** ... **GTCCGCA** **GAA** **GGTTGT** **TGAAGGTTAAGG** **GAACCA** **GAGAT** **ATAGCCGAT**  
10 **GGACCA** **CCCT** **CGGCGAAGCAACAT** **GGGA** **CACT** **CAAA** **GGTTGC** **TGAAGGTTAAGG** **CGGT** **TCAGAGA** **CAACCA**  
1: ..... **ATGCA** **GAA** **TGAT** **CTGTAAT** **GGAA** **CACT** **CAAA** **GGTTGC** **TGAAGGTTAAGG** **CGGT** **TCAGAGA** **CAACCA**

230 **GTGAGCTT** **CAGAGGAGTTTACG** **CAAAAGGATTTGGGGTAAATTTGGGTTGGTGGATTCAG** **CAGAGGCTTA** .....  
 DREB2A. nuc  
 227 **GTAAGCTT** **TACAGCAGTTTACAGAAAGCATTTGGGGTAAATTTGGGTTGGTGGATTCAG** **CAGAGGCTTA** .....  
 DREB2B. nuc  
 229 **GTGACAT** **TACAGCAGTTTACAGAAAGCATTTGGGGTAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2C. nuc  
 194 **GTGACAT** **TACAGCAGTTTACAGAAAGCATTTGGGGTAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2E. nuc  
 203 **GTGGCTT** **TACAGCTTTTCGACAAAGGCTTTGGGCGAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2D. nuc  
 119 **GCTGCTT** **CAAGCTTGTACCAACGCGGATTTGGGCGAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2G. nuc  
 95 **GTCACTT** **CTCGGATTTAGCAACGCGGATTTGGGCGAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2F. nuc  
 77 **GTGACG** **ATCCGTGAGTTCAGCAACGCGGATTTGGGCGAAATTTGGGTTGGTGGATTCAG** **TCAGAGCCGA** .....  
 DREB2F. nuc

PREB2A.nuc 304.....GGCTTTGGCTTGGTAACTTTCCTACTGCTCTAAGAAGCTGCTTCTGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2B.nuc 301.....GACTTGGGCTTGGTATTTTCTAATCCGCGAARAGCTGCTCCGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2C.nuc 283.....GGTCTGGGCTTGGTATTTTCTAATCCGCGAARAGCTGCTCCGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2H.nuc 268.....AGTTTGGGCTTGGTATTTTCTAATCCGCGAATGGAAGCTGCTATGAGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2E.nuc 288TAGTCGTAGTAACGGCTTTGGGCTTGGACGTTTGGCTACGACGCGAAGCTGCTATGAGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2D.nuc 193.....GTCTTTGGGCTTGGACGTTTGGCTACGACGCGAAGCTGCTATGAGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2G.nuc 169.....GTCTTTGGGCTTGGACGTTTGGCTACGACGCGAAGCTGCTATGAGCTTATGATGAGGCTGCTAAAGCTATG  
 PREB2F.nuc 151.....GACTTGGGCTTGGACGTTTGGCTACGACGCGAAGCTGCTATGAGCTTATGATGAGGCTGCTAAAGCTATG

376 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGGCTGATGCGCTCT** .. **GAGGATACGAGTACCTCAAGTCACT**  
 373 **TATCGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 355 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 373 **TATCGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 340 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 373 **TATCGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 373 **TATCGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 265 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 241 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**  
 223 **TATGGCTCTATGGCTCGTCTTAAATWGGC** ..... **TGAGCTGTTGGTCT** .. **GAGTAACTAGTACGCTAGTACAT**

[illegible]

Fig. 7-2

[illegible]

Fig. 8

DREBIA 1: ...MNSFSAFSEMFSGDYESSVSSGGDYIPTASSCPKKKAGRKKKPRETRHPPIYRGVRR  
DREBIB 1: ...MNSPFAFSEMFSGDYEP...QGGDYCPATAISCPKKKAGRKKKPRETRHPPIYRGVRR  
DREBIC 1: ...MNSPFAFSEMFSGDYESPVSPPKLAISCPKKKAGRKKKPRETRHPPIYRGVRR  
DREBID 1: MNPYISTPDSFLSISDHRSPVSDSSKCSKPKKAGRKKKPRETRHPPIYRGVRR  
DREBLE 1: .....NENDITVAENKPKKAGRKKKPRETRHPPIYRGVRR  
DREBIF 1: .....MNNDITIAEMRPKKKAGRKKKPRETRHPPIYRGVRR

DREBIA 57: RNSGKNVCEVREPKKRIINLCTFOTAEAAARAHNDVAALALGRSACLNFADSAVRLRI  
DREBIB 54: RNSGKNVSEVREPKKRIINLCTFOTAEAAARAHNDVAALALGRSACLNFADSAVRLRI  
DREBIC 57: RNSGKNVCEVREPKKRIINLCTFOTAEAAARAHNDVAALALGRSACLNFADSAVRLRI  
DREBID 60: RNSGKNVCEVREPKKRIINLCTFOTAEAAARAHNDVAALALGRSACLNFADSAVRLRI  
DREBLE 36: RQDKNVCEVREPTHQRRVILCTPTADAAARAHNDVAALALGRSACLNFADSAVRLPV  
DREBIF 36: RQDKNVCEVREPTHQRRVILCTPTADAAARAHNDVAALALGRSACLNFADSAVRLPV

DREBIA 116: PESTCAKDIOKAARAEHALAFQDEMCDATDHG.FDNEEPLVEAIYTAE.....QSENAF  
DREBIB 113: PESTCAKDIOKAARAEHALAFQDETCDTTNEGLDNEEPLVEAIYTPE.....QSEGAR  
DREBIC 116: PESTCAKDIOKAARAEHALAFQDEMCHMTDAGLDNEEPLVEAIYTPE.....QSEODAF  
DREBID 119: PETTCPKDIOKAASBAAMAGNETTEGSKTA.AEAEBAAGCGVREGERRAEENGGVF  
DREBLE 95: EASTDPDTRRTAASAAEMRPPEPFGTGTVLPSASEPDT.....  
DREBIF 95: PESNDPDVIRRVAAEAAEMRPVDLESGITVLPACGDDVDLGFSGSGSGSGSEERNSS

DREBIA 169: VNDEEAMFEMP SLLANMAEGMLLPSPVQNNHH.....EVDGDDDDVSLMSY..  
DREBIB 167: VNDEETMFGPTLLDNNAGGLPPSPVQNNHHY.....DGECDGDVSLMSY..  
DREBIC 170: VNDEEAMLGSSLLDNNAGGLPPSPVQNNHF.....DVEGDDDDVSLMSY..  
DREBID 177: VNDEEALLGPNPFENNAGGLPPSPVQNNHH.....DFDGVGDVSLMSFDE  
DREBLE 135: .....DEGVAGNMRLAEPLMSPPSYIDNN..TSVVDESMCYEDISLMSY..  
DREBIF 154: SYGFGDYEEVSTMMRLAEGPLMSPPSYMEDNTPTNVYTEEEMCYEDISLMSYRY

Fig. 9

DREB2A 1:MAVYDQSGDRNRTOIDTSRKRKSRGRDGTVAERKRMKEYNEIVSEVSTX.....KRVVPAKSGKKGCKNKGKGG  
DREB2B 1:MAVYEQTG.....TEQPKRKSRARAGGLTVADREKRMKEYNEIVEASAVKEG...EKP KRVVPAKSGKKGCKNKGKGG  
DREB2C 1:MPSE.....IVDRKRKR.....GTRDVAEIRQRMKEYNEQIEAESCIDGGEPKSIKPPPKESRKGCARGKGG  
DREB2D 1:.....MEKEDNGSKQSSASUVSSRRRRRVVEPVEATLQWEEEGGLARABRVQAKSGKKGCKNKGKGG  
DREB2E 1:.....MEKSSSSKQ.....MEKSSSSKQ.....WKGPARGKGG  
DREB2F 1:.....MEEEQPPAKKRNNGSRKKGCKNKGKGG  
DREB2G 1:.....RKRKR.....GTRDVAEIRKRMKEYNEQTEADSCIDGGGSKPIRKAPPKRSRKGCNKGKGG  
DREB2H 1:MP.....RKRKR.....GTRDVAEIRKRMKEYNEQTEADSCIDGGGSKPIRKAPPKRSRKGCNKGKGG

DREB2A 72:PERISGCFRGVRORIWKWVAEIREPN.....RGRNLNLGTFPTAQEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2B 71:PDNSHCFSRGVRORIWKWVAEIREPK.....IGRLNLGTFPTAEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2C 65:PENGICDYRGVRORRWKVAEIREPD.....GRLNLGTFSSSYEAALAYDEARAKMYGPIARLNPFRSD...  
DREB2D 35:PDNASCTYKRGVRORTWCKWVAEIREPN.....RGRNLNLGTFPTAEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2E 63:PERPVCRFGRVRORTWCKWVAEIREPN.....RGRNLNLGTFPTAEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2F 21:PNALCOYRGVRORTWCKWVAEIREPK.....KRLNLGTFPTAEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2G 27:PENATCTFRGVRORTWCKWVAEIREPN.....RGRNLNLGTFPTAEERASAYDEARAKMYGPIARLNPFRSD...  
DREB2H 60:PENGICDYTCVRORTWCKWVAEIREPG.....RGRNLNLGTFSSSYEAALAYDEARAKMYGPIARLNPFRSD...

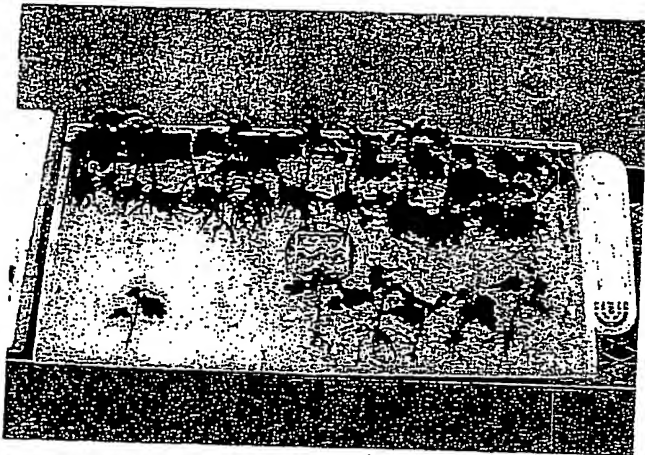
DREB2A 138:.....ASEVSTSSQSEVCTVETPGCVK.....VKTEBDDCEBCKPPSG...GVEPMYCLN.....GAHEKRGV  
DREB2B 137:.....GSEFTSTSSQSEVCTVENKAVCGDVCKKHEDTDCESNPFQILDVREESCCTRPDSCVGHQDMNSSL  
DREB2C 135:SSATAATVSGSVTAFSESEVCAREDTNASSGFGVCKLEDSCDEIVLLDSSQICKELKKEE.....VREHNLA  
DREB2D 102:.....SYPKTASSPASQTPS  
DREB2E 138:.....GGRKXDEEAESSGYWLETNKAGNGVETEG.....GKDYVVYN.....  
DREB2F 89:.....TRPSLSNSQRFKWPSPR.....XPFISMPSCGMLNVAQPSVHIQORLEELKXTGL  
DREB2G 95:.....QVVVNRLNLSFGSGSGSWAYNKKLDVHGLDGLGQASCGRGSCSERSFLQEDDD  
DREB2H 126:.....LQARLLHFLMLNLFVHVRIQMDLVLVS.....LTSR.....

DREB2A 196:KADKHWLSEFEHNYWSDILKEKX...QKEQGIIVETCQQQQQ.....DSISVADYGP...NDV...DQSHLDS.....SDM  
DREB2B 207:NYD...LLEFEQYWGQVLQEKEXKQEEESIQQQQQQQQQQLOPDLITVADYGPWNSNDIVNDQTSWDP.....NEC  
DREB2C 208:GFG.....IGQDSKRETLDAWLMNGNEQEPLEFGVDETFD...INELGILNDNNVSGQETWQYQVDRHPNFSYQTQ  
DREB2D 118:..SNTGCKSSSDS.....ESPCSS...NEMSSCG.....RVTEISWEHINVDLPVMD...S  
DREB2E 177:.....ESKNTSFLDEKTSKGETDNMFEGGQKKPEIDLTEFLQGLILKDN.....SA  
DREB2F 142:LSQSYSSSSST.....ESKNTSFLDEKTSKGETDNMFEGGQKKPEIDLTEFLQGLILKDN.....SA  
DREB2G 153:HSNRCSSSSGSNLCWLLPKQSDSQDETUNATSYGEGGGGTTFTSTNLKPKNLSQNYGLYNGAWSRPLVGQEK  
DREB2H 160:.....ISKMSPI.....TALVKLGRY.....

DREB2A 259:FDVDELLRDNGDDVFAGLNQDRYPGNSVANGSYRPESQQSGFDPLOSLNYGIPPPQLEGKXGNGFFFDLSYLDLEN  
DREB2B 279:FDINELLGDN.....EPGPHQSQDQ.....NHVNSGSYDLPLHLEPHDG.HEPNGLSSLDI..  
DREB2C 278:FPNSNLLGSN.....PNEIAQPGVDYCPYVQPSDMENYIGIDLHRRFNDLDIQDLDFGCKDVHGST..  
DREB2D 164:SIWEEATMSLGPVWVEGDN.....DISR.....FDTGISGGY.....SNWQSFHSPL..  
DREB2E 208:YSYDRFK.....LDNCLLYNEPQSSSYHQGGGFDSEYEFPR..  
DREB2F 204:EPSEVAECHSPPPWNEQETGSPFRTEPNFSDWTLEMPKSETTMOFSSNFGSYDFEDDVSPFSIWYIGSLD..  
DREB2G 231:KTEHDVSSCGSSDNKESMLVPSGGERMHRPELEERTGYLEMDLLEIDDLGLLIGKNGDFKXNCCERFQHPWNW  
DREB2H .....



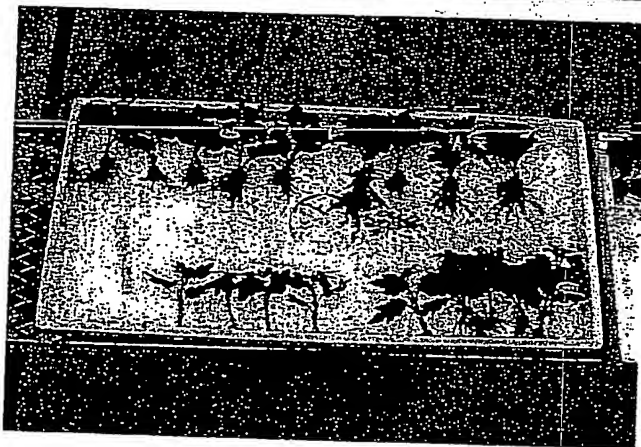
Fig. 10



strain 9



strain 10



non-transformant



Fig. 11

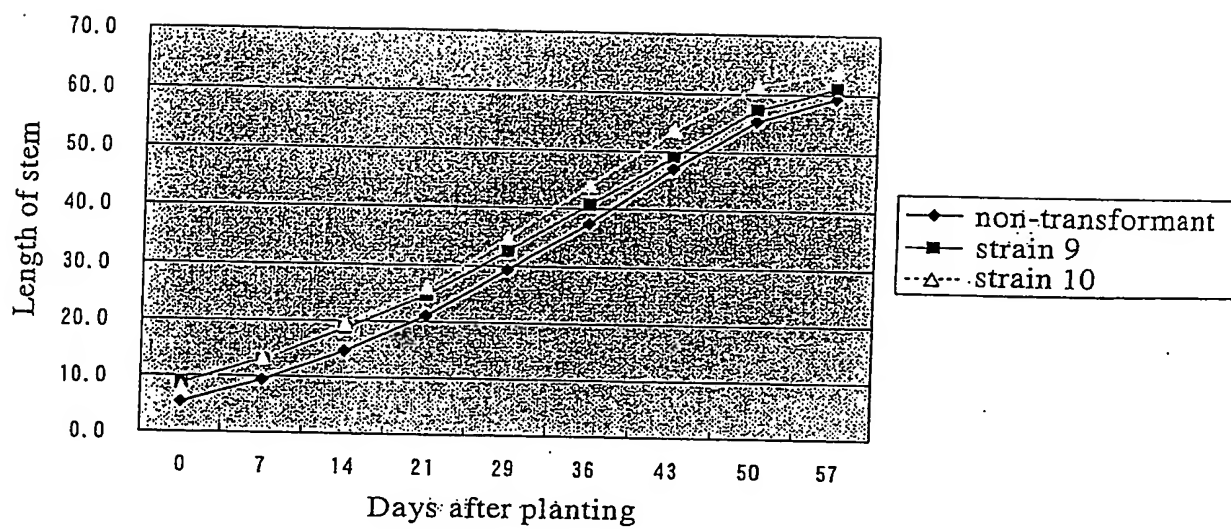
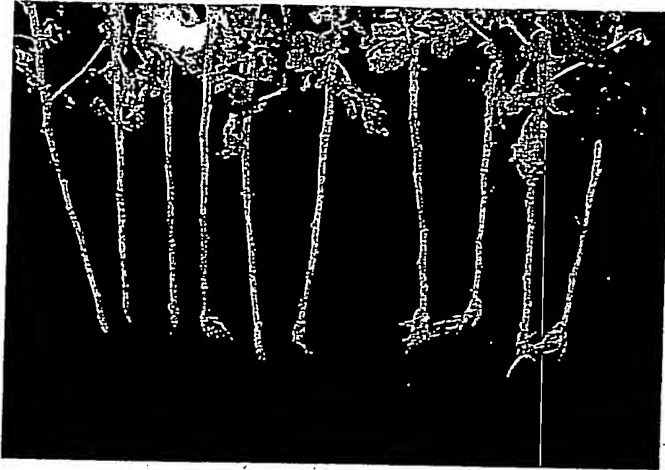
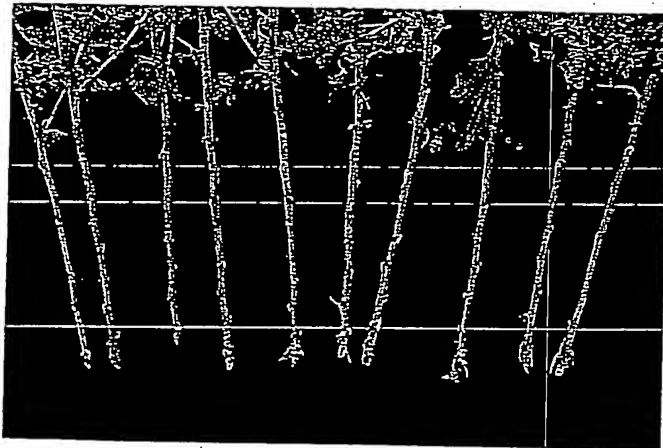


Fig. 12



strain 9



strain 10



non-transformant